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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ado50295 Escherich	ADO50295	12	1901	97.2	1284.6	18
Adil6137 Escherich	AULIBI37	12	667T	91.4	/ 87T	11
ACaly29/ Prokaryot	ACAL929/	· a	5527	97.4	1001	
ADKIZSI4 UNA encod	#ICZIAGN	, (1299	27.1	100	1 1
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Aee75418 R. coli B	AEE75418	15	1901	97.4	1287.8	14
Aed50819 Escherich	AED50819	14	1901	97.4	1287.8	13
Ado50297 Escherich		12	1901	97.4	1287.8	12
Adc87744 DNA encod	ADC87744	10	1901	97.4	1287.8	11
Ada19449 E. coli K	ADA19449	8	1901	97.4	1287.8	10
Aad25463 Escherich	AAD25463	0	1901	97.4	1287.8	9
Ado50303 Escherich	ADOS0303	12	1323	99.5	1315.6	00
Ado50301 Kangaroo	ADO50301	12	1323	99.5	1315.6	7
Aee75412 E. coli B	AEE75412	15	1323	100.0	1322	0
Ado50291 Escherich	AD050291	12	1323	100.0	1322	. от
Ada19445 E. coli B	ADA19445	8	1323	100.0	1322	4.
Aad25460 Escherich	AAD25460	0	1323	100.0	1322	w
Aad36473 Escherich	AAD36473	0	1323	100.0	1322	N
Aac88885 Escherich	AAC88885	v	1323	100.0	1322	
Description	ID	DB B	Length	Match	Score	No.
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7 92.1	3 94.7	3 94.7	94		95.5	95					5 95.7		-			96.9	97.0	97.0		-	97	97	97.0	97	8 97.1	5 97.2
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AED50824	ACC57673	AAD06832	AED50817	AEE75422	ADA19452	AAD06831	ACC57672	AAA28216	ABE75420	ADO50299	ADC87742	ADW76362	AAC68299	AEF15218	ADL16138	ADL02197	AAC68294	AAC68300	AAC68295	AAC68297	AAC68296	AAC68298	AE875417	ADO50296	ADL16139	AEE75416
Aed50824 Escherich	Acc57673 Escherich	Aad06832 E. coli a	Aed50817 Escherich	Aee75422 E. coli B	Ada19452 E. coli K	Aad06831 E. coli a	Acc57672 Escherich	Aaa28216 E. coli a	Aee75420 E. coli B	Ado50299 Escherich	Adc87742 DNA encod	Adw76362 Phytase A	Aac68299 SV40/APPA	Aef15218 Escherich		Adl02197 DNA encod	Aac68294 Lama2/APP	Aac68300 Lama2/APP	Aac68295 R15/APPA	Aac68297 R15/APPA	Aac68296 R15/APPA	R15/APPA	Aee75417 E. coli p		Adl16139 Shigella	Aee75416 E. coli p

ALIGNMENTS

RESULT 1

ID AAC88885 standar XX AC AAC88885; XX XY DT 07-MAR-2001 (fi XX Escherichia coli XX DS Escherichia coli XX DS OS DS	standard; DNA; 1323 BP.; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;
	oli B phytase enzyme nucleotide sequence.
	nia coli.
	728-A1.
	300.
PF 25-MAY-2000;	000; 2000WO-US014846.
PR 25-MAY-1999;	99; 99US-00318528.
	(DIVE-) DIVERSA CORP.
PI Short JM,	Kretz KA;
DR WPI; 2001-112081 DR P-PSDB; AAB37892 XX	WPT, 2001-112081/12. P-PSDB, AAB37892.
	Improving the nutritional value of phytate-containing foodstuffs, phytase enzymes which catalyze the liberation of inorganic phosphthe phytates.
	Claim 2; Fig 1; 147pp; English.
	The present sequence encodes a phytase enzyme from Escherichia co The enzyme catalyses the liberation of inorganic phosphate from t phytate in phytate-containing foodstuffs and can thus be used to the nutritional value of phytate rich ingredients

the phytates. Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from

The present sequence encodes a phytase enzyme from Escherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate in phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients



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WO200189317-A2 /*tag= Location/Qualifiers /product= .1323 "E. coli phytase protein"

29-NOV-2001. 15-MAY-2001; 2001WO-US015764

25-MAY-2000; 2000US-00580937

(DIVE-) 2002-164149/21. DIVERSA Kretz KA, CORP ó donoghue

AAE22836

New dietary aids comprising sustained release biocompatible compositions, comprise agent that assists in digestion, useful for delivering enzymes, therapeutics, medicine or agents to an organism.

Disclosure; Fig 1; 89pp; English.

The present invention relates to novel dietary aids comprising sustained release biocompatible composition which comprises an agent (enzymes such as phytase, amylase, esterase, protease) that assists in digestion. The biocompatible composition is effective upon oral consumption and release in the digestive tract of a subject. The dietary aids are useful for delivering enzymes, therapeutics, medicine and agents to an organism. The

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                        CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG
                                                                           GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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                  New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; nutritional value; feed treatment process; thera; thermal tolerance; growth performance; alcoholic drink; biopulping non-alcoholic drink; biobleaching; B phytase; ds.
                                                                                                             WPI; 2002-083108/11.
P-PSDB; AAE15806.
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The patent discloses recombinant bacterial phytase from Escherichia coli CC K12 appA phytase. The enzyme has phytase activity and improved thermal CC tolerance when compared with wild-type phytase. It has improved protease CC stability at low pH. The recombinant phytase is useful for improving the CC nutritional value of phytate-containing foodstuffs and subsequently CC improving the performance of an organism that consumes it, in CC vitro purposes related to research, discovery and development. They are CC also used for generating recombinant digestive systems, in from containing and paper industry and development. They are CC used for generating recombinant digestive system life forms, for CC the use of moulds, grains and/or plants, in biopulping and bio-bleaching CC where a reduction in the use of environmentally harmful chemicals that CC are traditionally used in the pulp and paper industry is desired and in CC the reduction or possible elimination of the need for mineral CC supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed.

The present sequence is a DNA encoding E. coli B phytase protein
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Best Local Similarity
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  13-AUG-1997;
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n enhancement; transgenic; thermal tolerance; protease stability
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The invention relates to an isolated Escherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids conditication from W68E, Q84W, A95P, K97C, S168E, R180Y, N226C or Y277D. CC Also included the E. coli appA gene ADA19449 (or an oligonucleotide derived from it) or its mutant sequence ADA19452, expression vectors, host cells, a method of improving nutritional value of a phytate-containing foodstuff by contacting the phytate-containing foodstuff with containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in the phytate containing a microbial phytase (comprising culturing the plant cell, plant part or containing a foodstuff), a method to produce an animal feed containing a feed composition for animals (comprising the plant seeds, plant cells, plants parts or plants in admixture with a phytate-containing containing a plant parts or plants in admixture with a phytate-containing comprising administering to the human or animal able to benefit from comprising administering to the human or animal the plant seeds, plant cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence containing a phytase enzyme, a transgenic non-human organism whose genome containing phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The containing the phytate mander to contain an expression of animal feed and for enhancing digestion in humans and animals. The present sequence encodes E. coli B wild-type phytase.
                                                                                                                                                                                                                     Query Match
Best Local S
Matches 1323
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O' Donoghu
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(KRET/)
(GRAY/)
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) KRETZ K A.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O' DONOGHUE E.
) MATHUR E J.
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially
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P-PSDB;
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DB; ADO50292.
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BARTON N R.

GARRETT J B.

O'DONOGHUE E.

MATHER E J.
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                                      CGCACGCCAGAGGGTTGCCCGCAGCCGCGCCCACCCCCGTTATTGGATTTGATCATGGCAGCG
                                                                                                   GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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pharmaceutical; fertilizer; cramp; cell culture; osteoporosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1323; Conserv
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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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(KRET/)
(GRAY/)
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(ODON/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytase;
phytate;
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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease ct stability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytase rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant mammals such as pigs, goats, doves, parrot, etc., CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in datary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Scherichia coli W phytase mutant DNA. Note: The present CC scherichia coli B phytase DNA ADO50291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 1319;
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P-PSDB; ADO50292, ADO50304.
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(KRET/)
(GRAY/)
(BART/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
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                                                                                                                                                                                   Query Match
Best Local Simi
Matches 1293;
                                                                                                                                                                                                                                                 Sequence
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
                                                                  The invention relates to an isolated Escherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from W68E, 084W, A95P, K97C, S168E, R180Y, N226C or Y277D. Also included the E. coli appA gene ADA1949 (or an oligonucleotide derived from it) or its mutant sequence ADA19452, expression vectors, host cells, a method of improving nutritional value of a phytate-containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in the phytate-containing a microbial phytase (comprising culturing the plant cell, plant part or plant under conditions where the nucleotide sequence is expressed and plant the phytate than the phytase catalyzes.
  converting the plant cells, plants or plant into a composition for animal feed), a feed composition for animals (comprising the plant seeds, plant cells, plant parts or plants in admixture with a phytate-containing
                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Bscherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.
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(GRAY/)
(BART/)
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DB; ADA19450.
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) KRETZ K A.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O' DONOGHUE E.
) MATHUR E J.
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       GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                               GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                                                                       13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
                                                                                                                                                                                                                                24-MAY-2002; 2002US-00156660.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
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                                           ; 97US-00910798.

; 99US-00259214.

; 99US-00291931.

; 99US-00318528.

; 2000US-00580515.

; 2001US-00866379.
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Short JM,
Mathur EJ;
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                                                     Barton NR,
                                                     Garrett
                                                     JB,
                                                     O' donoghue
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WPI; 2003-787039/74. P-PSDB; ADC87745.

New nucleic acid encoding a polypeptide having phytase activity, useful in improving the feeding value of phytate rich ingredients or as an aid in phytate digestion.

Example 1; SEQ ID NO 3; 113pp; English.

The invention discloses a new isolated or recombinant nucleic acid which concleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, a phytase message in a cell, a heterodimer comprising the translation of a second domain, an array comprising immobilised polypeptide and a acid, a hybridoma comprising an antibody that specifically binds to the polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, a feed composition, a soybean meal, isolating or identifying compressing an anti-phytase antibody, producing a recombinant polypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, a modulator, whole cell engineering of new or modified the resistance of the phytase polypeptide to enzymatic inactivation in a digestive system and processing of corn and sorghum kernels. The phytase activity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or casa an aid in phytate digestion. The sequence presented is the DNA

Sequence 1901 BP; 474 A; 499 C; 499 G; 428 T; U; 1 Other;

δ 밁 S 片 S 밁 Ś 밁 S 밁 8 Query Match
Best Local Similarity
Matches 1293; Conserv 548 361 488 301 · CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 428 368 248 241 181 308 121 188 61 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA GTGCGTGCTCCAACCAAGGCCAACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA ATGAAAGCGATCTTAATCCCATTTTTATCTCTCTGATTCCGTTAACCCCCGCAATCTGCA GCCTTCGCCGCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 97.4%; milarity 99.5%; Conservative Score 1287.8; Pred. No. 0; 0; Mismatches <u>,</u> DB 10; 7; Indels Length 1901; 0 Gaps 360 607 420 547 300 487 427 240 367 307 247 60

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TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG

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           AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; gene; ds.
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                                                                                                                          The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease estability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 apph phytase DNA.
                                                     Matches 1293;
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Short JM,
Mather EJ;
                                                                                                                                                                                                                                                                                                                                                                                Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHOR/)
(KRET/)
(GRAY/)
(BART/)
                                                                                                       Sequence 1901 BP; 474 A; 499 C; 499 G; 428
                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 7; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ODON/)
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                                                                 Local Similarity
  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) SHORT J M.
) KRETZ K.
) GRAY N N.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
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Kretz K,
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2000US-00580515.
2001US-00866379.
                                                      Conservative
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99US-00259214.
99US-00291931.
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                                                   Score 1287.8;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garrett
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                                                                             DB 12;
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                      CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC
                                                                  CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                                                                                                                                                                                                                                                                                                        CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG
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                                                                                                                                                                                                             TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
                                                                                                                                                                                                                                       TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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   CAGATGCGT
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The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, fould degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also

of an animal

for

Example 1;

SEQ ID NO 3; 104pp; English.

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25-MAY-2000;
24-MAY-2001;
24-MAY-2001;
                                                                                                                                                                                                       New isolated or recombinant nucleic acid encoding phytase enzymes, useful as foodstuff, and for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal.
                                                                                                                                                                                                                                                                                                                WPI; 2005-733851/75.
P-PSDB; AED50820.
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13-APR-1999;
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3-phytase;
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GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
MATHUR E J.
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appA gene.
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99US-00259214.
99US-00291931.
99US-00318528.
2000US-00580515.
2001US-00866379.
2002US-00156660.
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/product= "Escherichia coli phytase protein"
/transl except= (pos:401. .403,aa:Arg)
/EC_number= "3.1.3.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a polynucleotide encoding the Escherichia CC coli phytase appA, which was modified to produce a thermostable protease CC resistant phytase which constitutes the novel enzyme of the invention. CC The present invention relates to a novel formulation, comprising at least cone polypeptide having phytase activity, where the polypeptide is a CC modified sequence (AEE75421) derived from the Escherichia coli K-12 appA CC phytase (AEE75419). The modification of the enzyme, comprising a series CC the protein. The specification also claims a pharmaceutical composition, a kit; an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing pollution and increasing mutrient availability in an environment or environmental sample by degrading environmental phytic acid. The novel enzyme is a dietary complement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful for preventing muscle cramps. The method is useful for reducing pollution and increasing nutrient availability in an environment or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1901 BP; 474 A; 499 C; 499 G; 428 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 7; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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P-PSDB; AEE75419.
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                        GCCTTCGCCGCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG
                                                                                                      CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA
                                                                                                                                                                 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG
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GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                                                CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAAACAGGCGAA
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Pred. No. 0;
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ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT 1487
              ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTTGAGAT 1300
                                                                   CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                                       CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC
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                                                     CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                         CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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ABK12514
ID ABK12514 standard; DNA; 1299 BP.

XX
AC ABK12514;
XX
DT 05-JUN-2002 (first entry)
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DB DNA encoding phytase associated protein
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Phytase; gene; ds.
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Matches 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 97.4%;
Best Local Similarity 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel phytase gene, a recombinant phytase gene and their uses. This sequence encodes a phytase associated protein, described in the invention
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P-PSDB; AAU77775.
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                            GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC 600
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/product= "Phytase associated protein"
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Pred. No. 0;
0; Mismatches 6;
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Search completed: June 14, 2006, 10:31:32 Job time : 903.103 secs

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601 CTTABARCGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC	Qy 481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	Oy 361 GCCTTCGCCGCCGGCGGCTGGCACTGACTGTGCATAACCGTACATACCCAGGCAGATACC	Qy 241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGATTGCTGGCGAAAAAAGGGCTGCCCG 300	ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC	61 61 121	Query Match 100.0%; Score 1322; DB 2; Length 1323; Best Local Similarity 100.0%; Pred. No. 0; Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AIGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	SOURCE Unknown. ORGANISM Unknown. Unclassified. Unclassified. Unclassified. Inclassified. Inclassified.	RESULT 2 AR127818 LOCUS AR127818 DEFINITION Sequence 1 from patent US 6183740. ACCESSION AR127818 VERSION AR127818.1 GI:14115480 KEYWORDS .

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Short, J.M. and Kretz, K.A.
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Diversa Corporation; San Diego, CA
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Short,J.M., Kretz,K.A., Gray,K.A., Barto O'Donoghue,E. and Mathur,E.J.

O'Donombinant bacterial phytases and uses Patent: US 685365-A 1 15-FEB-2005;

Diversa Corporation; San Diego, CA

Location/Qualifiers
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CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTGGATTTGATCATGGCAGCG
                                         GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                                      GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                           GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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Escherichia coli
Bacteria, Proteobacteria,
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Sequence 1 from Patent WO0071728,
AX052713
AX052713.1 GI:12226903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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AX338966 1 GI:18129102
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                                            TTCGCTCAGAGTGAGCCGGAGCTGAAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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Conservative 0
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/db_xref="taxon:562"
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Recombinant bacterial phytases and uses thereof Patent: WO 0190333-A 1 29-NOV-2001; DIVERSA CORPORATION (US)
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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S 밁 Ś 맑 ঠ 닭 S 밁 Ś Query Match Best Local Similarity Matches 1323; Conserv 241 181 121 121 181 61 61 μ μ GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA ATGAAAGCGATCTTAATCCCATTTTTATCTCTCTGATTCCGTTAACCCCCGCAATCTGCA GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 100.0%; ilarity 100.0%; Conservative 0 0; Score 1322; Pred. No. 0; 0; Mismatches DB 2; 0; Indels Length 1323; o, Gaps 300 180 120 240 240 180 60 120 8 0

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Short, J.M., Kretz, K.A., Gray, K.A., Be O'Donoghue, B. and Mathur, B.J.
Recombinant bacterial phytases and us Patent: US 685365-A 7 15-FEB-2005;
Diversa Corporation; San Diego, CA Location/Qualifiers
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AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                             AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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Query Match 97.4%; Score 1287.8; DB 2; Length 1901; Best Local Similarity 99.5%; Pred. No. 0; Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0; 1 ATGADAGCGATCTTAATCCCATTTTATCTCTTCTGATTCCGTTDACCCCGCAATCTGCA 60	source 11901	TITLE RECOmbinant bacterial phytases and uses thereof JOURNAL Patent: WO 0190333-A 7 29-NOV-2001; DIVERSA CORPORATION (US) EATURES Location/Qualifiers	REFERENCE 1 AUTHORS Short, J.M., Kretz, K.A., Gray, K.A., Barton, N.R., Garrett, J.B. and O'Donoghue, E.	SOURCE Escherichia coli ORGANISM Escherichia coli Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	ON Sequence 7 from Patent W00190333. NX356572 AX356572.1 GI:18621059		Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	QY 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGGCCG	OY 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	OY 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	Qy 961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020	Qy 901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGAGATTACCCACTTCAGTACTG 960	Qy 841 CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900	Qy 781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840	CY 721 GAGATATTCTCCCTGCAACAAGCACAGGAATCCCGGAGCCGGGGTGGGAACGATCACC 780	ono Annostanovoccantasioictatianccogifacagicicacicanicaniacitanca
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1208 ACGCTTACCGGATAACAGCCAGTGGATTCAGGTTTCCAGACTTTACAG 1327 1208 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTCTCCAGACTTTACAG 1327 1208 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140 11081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140 11081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1327	TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG		841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCGCCCCCCTTATTGGATTTGATCATGGCAGCG 900	781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840 	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780 	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600 	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGAGGGTCAATTGCTGACTTTACCGGGCAT 540	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480 	361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 360 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 300	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	188 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGGAATCTGCA 247

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Asp304 of Escherichia coli acid phosphatase is involved in leaving
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Dassa, J., Marck, C. and Boquet, P.L.
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YLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGG
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note="created by site direct
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Pred. No. 0;
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TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA

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1208 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGATGAACTGGTGTTTGAACGCTTGG 1267 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	1028 CGCACGCAAGAGGTTGCCCGCAAAAACAGGCGTATTGACACATTACCCACTTCAGTACTG 1087 901 TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGACATTACCCACTTCAGTACTG 960		GACATTACCAACGCCATCATTACTCAAAAACTTGAAAAACTTGAAACTTGTGC 428 GACATTACCAACGCCAGCGTCTGGTAGCCGACGAATTGCTGGCGAAAAAGGGCTGCCCG 301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGGCTGCCG 487 301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA 488 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCTACC	
Query Match 97.4%; Score 1287.8; DB 15; Length 110000; Best Local Similarity 99.4%; Pred. No. 0; Matches 1292; Conservative 0; Mismatches 8; Indels 0; Gaps 0; Qy 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	3600001 3700001 3800001 3900001 4100001 4200001 4200001 4300001 4400001 4600001 4600001	U00096_19 1900001 2010000 U00096_20 2000001 2110000 U00096_21 2100001 2210000 U00096_22 2200001 2310000 U00096_23 2300001 2410000 U00096_24 2400001 2510000 U00096_25 2500001 2510000 U00096_26 2600001 2710000 U00096_27 2700001 2810000 U00096_28 2800001 291000 U00096_29 2900001 3110000 U00096_30 3100001 3210000 U00096_31 3200001 3110000 U00096_33 3300001 3110000 U00096_34 3400001 3510000	r into 47 fragmen Begin 1 100001 2000001 300001 4000001 500001 7000001 1000001 11000001 1200001 1200001 1300001 15000001 15000001 15000001 15000001	Db 1328 CAGATGCGTGATAAAACGCCGGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1387 Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCCAGGATGTGTTCGTTGGCAGGTTTTACGCAA 1260

1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG 1140		961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020 	901 TTGACGCCCATCCACCGCAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960 	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900 	781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840 	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC 780 	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	601 CTTABACGTGAGABACAGGACGABAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660 	541 CGGCAAACGGGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600 	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540 	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480 10260 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 40319	361 GCCTTCGCCGCGGGCTGGCACTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420 	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGGGTACCCCGTAAAACAGGCGAA 360 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG 300 	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGGNGGTGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180 	39900 TTCGCTCAGAGTGAGCCGGAGCTGAAAGCTGGAAAAGTGTGATTGTCAGTCGTCATGGT 39959
1292; Conservative 1 ATGAAAGGGATCTTAATCC	ery Match 97.4%; Score 1287.8; DB 15; Length st Local Similarity 99.4%; Pred. No. 0;	4300001 4400001 4500001 4600001 of 47) of Apo09	3900001 4000001 4100001 4200001	AP009048 ³ 5 3500001 3610000 AP009048 36 3600001 3710000 AP009048 ³ 7 3700001 3810000 AP009048 ³ 8 3800001 3910000	3100001 3200001 3300001 3400001	2700001 2800001 2900001 3000001	2300001 2400001 2500001 2600001	1900001 2000001 2100001 2200001	1500001 1600001 1700001 1800001	1100001 1200001 1300001 1400001	700001 800001 900001		ent Name Begin End 048 00 1 110000 048 01 100001 210000 048 02 200001 310000	RESULT 13 APPO09048 10 WPCOMMENT Sequence split into 47 fragments LOCUS APPO09048 Accession APPO09048	41100 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT		40980

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Short, J.M., Kretz, K.A., Gray, K.A., Barton, N.R.,
O'Donoghue, B. and Mathur, B.J.
Recombinant bacterial phyrases and uses thereof
Patent: US 685365-A 5 15-FBB-2005;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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                                                                  TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTTGCCAACTGGATAACGCG
                                                                                                                                   GCCTTCGCCGCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG
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Short,J.M., Kretz,K.A., Gray,K.A., Barto O'Donoghue,E. and Mathur,E.J.

Pacombinant bacterial phytases and uses Patent: US 685365-A 9 15-FEB-2005;

Diversa Corporation; San Diego, CA

Location/Qualifiers
                                                                                          Unclassified.
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10650.337 Million cell updates/sec
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BR520240 MILB12STM
AW036132 BST774510
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ALIGNMENTS

TITLS JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BJ074127/c LOCUS PEATURES DEFINITION ORGANISM source Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855 616 bp mRNA linear EST 29-SEP-2003 BJ074127 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL090j06 5', mRNA sequence. BJ074127 BJ074127.1 GI:17504316 Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i Xenopodinae; Xenopus; Xenopus. I (bases 1 to 616) I (bases 1, Terasaka, C., Mochii, M., Xenopus laevis (African clawed frog) Xenopus laevis http://xenopus.nibb.ac.jp. Location/Qualifiers Email: tshini@genes.nig.ac.jp The information of this clone Kohara, Y Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; /tissue_type="whole embryo" /dev stage="stage 25" /clone_lib="NIBB Mochii normalized Xenopus tailbud library" 1. .616 /organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="XL090j06" 411-8540, Japan 18 available through the following Ueno, , Z Shin-i, T.

Query Match Best Local Similarity

46.5**%**; 99.8**%**;

Score 614.4; DB 2; Pred. No. 8.3e-180;

Length

616;

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RESULT 2
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pacificus var. (
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              Evolutionary Biology
Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371
Fax: 00497071601498
                                                                                                AppaDB: an AcedB database
Pristionchus pacificus
Nucleic Acids Res. 32 (1)
                                                                                                                                                        Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                    survey sequence.
CL662734
CL662734.1 GI:5
                                                                           Contact: Sommer RJ
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Saccharum officinarum
Saccharum officinarum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                       3', mRNA sequence.
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This library was generated at Caltech, Pasadena, USA and sequenced at Vancouver, Canada. Seq primer: T7
Class: fosmid ends.
                         AGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 001 row; D column; 10
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Pax: 55 19 3788 1089
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Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13/Forward primer.
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The libraries that made SUCEST
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/db_xref="taxon:4547"
/clone="SCCCCL2001D10"
/lab_host="XL1Blue MRF'"
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Pred. No. 7.1e-153;
n. Mismatches 16;
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Schistosoma japonicum
Bukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Bukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 529)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
MCManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
Evolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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                 /tissue_type="Whole body"
//dev_stage="Adult worms"
/lab_host="Mouse and rabbit"
/clone_lib="Adult SjC 7/94"
/clone_lib="Adult SjC 7/94"
/clone_lib="Adult SjC 7/94"
/note="Weccor: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-XhoI-primer and synthesis was
primed with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EccRI linkers,
digsered with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hanzg@chgc.sh.cn
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/mol type="mRNA"
/strain="Chinese (Anhui) strain"
/db xref="taxon:6182"
/sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
a small percentage, 2% to 3%,
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Local

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Genomics and Genetics Institute, of Bioscience and Bioinformatics, Yongin, Kyeonggi, Korea
                                                                          Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T. Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                                                                                                                                                                                                                                                                                                                                 C9326092 595 bp mRNA linear EST 18-AUG-200 JMT1--05-B09.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA clone JMT1--05-B09, mRNA sequence.
                                                          Contact: Nahm B.H.
                                                                                                                                                                        clade; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                             CF326092.1 GI:33800445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCCC 1029
                                                                                                                                                      (bases 1 to 595)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      japonicum sequences."
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Pred. No. 1.2e-150;
0; Mismatches 5;
                    GreenGene Biotech Inc.; Division, MyongJi University
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RESULT 5 CF326092/c LOCUS

DEFINITION

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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

JOURNAL COMMENT

TITLE

REFERENCE

AUTHORS

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KEYWORDS
SOURCE
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CN762997/c
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VERSION
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                                                 IDOAAASDCO9RM1 / mRNA sequence. CN762997 CN762997.1 GI:
EST.
Acyrthosiphon pisum
Acyrthosiphon pisum
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82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nackdong"
/cultivar="Nackdong"
/db xref="taxon:39947"
/db xref="taxon:39947"
/clone="0MT1--05-B09"
/tissue_type="leaf"
/dev stage="14 days after germination"
/dev stage="14 days after germination"
/lab_host="E_coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; CDNA was inserted into landa UNI-ZAP XR vector at 5', end with EcoRI and 3', end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bhnahm@ggbio.com, bhna
Location/Qualifiers
                                                     GI:47536920
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                                                                                                     ApMS
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidodea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 895)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: CAGGAAACAGCTATGACC Plate: 5 row: C column: 9. Location/Qualifiers
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Contact: D. Tagu
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                                                                                                                                                                                                                                                                                               TCTCGGCGCGCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCATAACGCGCAAITTTAITTGCTACAACGCACGCCAGAGGITGCCCGCAGCCGCGCCCAC 872
TACGCCGCCGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGG 1232
                                                                               GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA 1172
                                                                                                                                                                                    AGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA 1112
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                                                 GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA
                                                                                                                                                         AGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: IDDANA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
/clone_lib="ApMS"
/clone_lib="ApMS"
/note="Vector:_pBS-SK minus; Site_1: EcoRI; Site_2: XhoI.
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/mal_type="mRNA"
/culfivar="developmentstage"
/db_xref="taxon:7029"
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CN754382/c
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Best Local Similarity
Matches 454; Conserv
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Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 868)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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CN754382
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                                                                                                 /clone_lib="ApMS"
/clone_lib="ApMS"
/note="Vector; pBS-SK minus; Site_l: EcoRI; Site_2: XhoI;
/note="Vector; pBS-SK minus; Site_l: EcoRI; Site_2: XhoI;
/note="Vector: pBS-SK minus; Site_l: EcoRI; Site_2: Department of Bcology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Bascription: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                            /dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Acyrthosiphon pisum"

/mol type="mRNA"

/culfivar="developmentstage"

/db xref="taxon:7029"

/clone="IDOAAA12DE01"
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                         33.2%;
Score 438.8; DB 8;
Pred. No. 6.1e-125;
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CN757565/c
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
FOR PRIMERS
FORWARD: CAGGAAACAGCTATGACC
Plate: 1 row: F column: 9.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Naphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 864)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
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CN757565.1 GI:47531488
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Contact: D. Tagu
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                           /clone="IDOAAAIDF09"
/tissue_type="whole insect"
/dev_stage="nymphs and adult
/lab_host="XL1-Blue"
                                                                                                                           /mol
/clone_lib="ApMS"
/note="Vector: pBS-SK minus;
                                                                                            /cultivar="developmentstage"
/db_xref="taxon:7029"
                                                                                                                                      organism="Acyrthosiphon pisum"
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Site_1:
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CGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT 408

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Matches 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTGTT
CGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                                        GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACCCT
                                                                                                                                                                                                                                                                                                                                                                                             GCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCTGGCG 1082
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                                                                 GGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAAT
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                                                                                                                                                                                                                                                                                        TCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAGCA 1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sample name: IDOAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c) "
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98.3%;
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Pred. No. 1.1e-123;
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PUBMED COMMENT SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 9 BE520240/c LOCUS REFERENCE DEFINITION JOURNAL TITLE AUTHORS 11115976
Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University 1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. BE520240 393 bp mRNA linear M11B12STM Arabidopsis developing seed Arabidopsis Arabidopsis thaliana (thale cress) Arabidopsis thaliana clone M11B12 5', mRNA sequence. BE520240 BE520240.1 GI:9778242 224 Biochemistry, Michigan State University, East Lansing, EST 19-MAR-2001 thaliana cDNA 3

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REFERENCE
AUTHORS
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VERSION
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AW036132
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Matches 388; Conser
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383 bp mRNA linear EST 18-MAY-2001 EST7274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036132.1 GI:5894811
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, T.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C.,
                                                    Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledon
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
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Fax: 517 353 9334
Email: benning@mgu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Bot
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                         GTCTCATTAACCGGTGCGGTAAGCCTCGCATCA 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
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/db_xref="taxon:3702"
/clone="M11B12"
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/mol_type="mRNA"
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Pred. No. 1.3e-108;
D; Mismatches 5;
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Generation of ESTs from tomato se
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Insti
Clemson University
100 Jordan Hall, Clemson, SC 296:
                                                                                                                                                                                                                                                                                                                61
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3 prime sequence.
                                                                                                                                                                                                                                                                                                                               CCAGGCAGATACGTCCAGTCCCGATCCGTTATTAATCCTCTAAAAACTGGCGTTTGCCA
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ATCAATGCTGACGGAGATATTTC
                 ATCAATGCTGACGGAGATATTTC
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                                                                                         ACCATCGGAACTCAAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGC
                                                                                                                                                     ATCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATT
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="quiescent seed"
/lab_host="XL1-Blue MRF'"
/clone_lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_Xho1; CLEE - Tomato Seed EST Library. Directionally clonals inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
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/clone="clemater"
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/cultivar="TA496"
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Pred. No. 1.3e-107;
0; Mismatches 0;
383
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ACCESSION VERSION RESULT 11 AW036134/c LOCUS DEFINITION SOURCE ORGANISM KEYWORDS Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. AW036134 1837-74510 tomato seed, TAMU Lycopersicon esculent CLEST274510 tomato seed, TAMU Lycopersicon esculent CLESTER23 similar to periplasmic phosphoanhydride precursor, putative, mRNA sequence.

AW036134 AW036134.1 EST. GI:5894813 linear EST 18-MAY-2001 sculentum cDNA clone phosphohydrolase

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ACCESSION
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                                                                   BU713769
BU713769
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BU713769
SJĀABUGOI Ādult SJC 7/94 Schistosoma japonicum cDNA similar to spļ p07102 ppa ECOLI PERIPLASMIC APPA PROTEIN PRECURSOR [INCLUDES: PHOSPHOANHYDRĪDE PHOSPHOHYDROLĀSE (PH 2.5 ACID PHOSPHATĀSE) (AP);
                BU713769
BU713769.1
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                                                  6-PHYTASE ], mRNA sequence.
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                                                                                                                                                                                                                                        ATCAATGCTGACGGAGATATTTC 730
                                                                                                                                                                                                                                                                                                              ACCATCGGAACTCAAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGC
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                                                                                                                                                                                                                                                                                                                                                                                  ATCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="quiescent seed"
/lab_host="XL1-Blue MRF'"
/clone lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site
/note="Vector: pBlueScript SK(-); Directionally of the part of the pBlueScript SK(-) at 5' end with
ECDNAs inserted into pBlueScript SK(-) at 5' end with
ECORI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="seeds"
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100.0%; Pr
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; Pred. No. 1.3e-107;
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.edu/orders/index.html
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Similarity

Conservative

Mismatches

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7.9e-97;

670 GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT 729

GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG

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SOURCE
ORGANISM
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2 (bases 1 to 531)

3 (bases 1 to 531)

3 (bases 1 to 531)

4 (bases 1 to 531)

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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementary DNA resource Nat. Genet. 35 (2), 139-147 (2003)
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Fax: 86-21-50801922
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                                                                                                                                                                                                                                               /tissue type="Mable body"
/fishes type="Mable body"
/lab_host="Moule sody"
/lab_host="Moule sody"
/lab_host="Moule sody"
/lab_host="Moule and rabbit"
/clone lib="Adult S[C 7/94"
/note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
rabbits at the Queensland Institute of Medical Research,
Rrismane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-XhoI-primer and synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
clones contain inserts that appear to be highly homologous
to sequences from salmonoid fishes, as determined by
homology comparisons using BLAST and by Southern
hybridization analysis to genomic DNA from salmon (Sigma
Chemical Co., St. Louis, MO) under stringent washing
conditions. The remainder of the clones appear to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hanzg@chgc.sh.cn
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/strain="Chinese (Anhui)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Schistosoma japonicum"
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                                                       26.4%;
                                                       Score 348.6;
Pred. No. 7.9
                                                                                                               DB 3;
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REFERENCE
AUTHORS
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Clone HBMSF1B4 5', mRNA 8
AA545747
AA545747.1 GI:2307026
EST.
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                                                                                                                                                                                                                                                                                     Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda,
Tel: 301-402-4877
Pax: 301-496-7157
Email: libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                       Jia.L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon, C., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., Waterston, R., Wilson, R. and Francomano, C. Washu-MGB/NHGRI EST Project Unpublished (197)
Contact: Libin Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                          primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482
                                                                                           /sex="Male and Remale"
/tissue_type="bone marrow"
/cell_type="stromal fibroblast"
/dev_stage="mixed"
/lab_host="XL1-Blue"
                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HBMSF1B4"
                                                              /clone_lib="Hun
/note="Vector:
 23.0%;
                                                         lib="Human Bone Marrow Stromal Fibroblast"
"Vector: pBluescript, Site_1: EcoRI; Site_2
Score 304.6; DB 1; Pred. No. 3.9e-83;
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Marrow Stromal Fibroblast Homo sapiens cDNA
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acyrthosiphon pisum

Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 706)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Mu
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                       Risk of contamination by bacterial sequences from obligatory (Buchhera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope PCR PRimers
FORWARD: CAGGAAACAGCTATGACC
Plate: 24 row: C column: 4.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5', mRNA sequence.
CN759004
CN759004.1 GI:475
                                                                                                                                                                                                                                                                                                                                                                                                            UMR B103P, BP 35327, P
Tel: +33.2.23.48.51.65
Pax: +33.2.23.48.51.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: D. Tagu
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                                                                                      /db_xref="taxon:7029"
/clone="IDDAAA24BC04"
/tissue_type="whole insect"
/dev_stage="nymphs and adults
/lab_host="XL1-Blue"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: IDOAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999;
                                                        /clone_lib="ApMS"
/note="Vector: pB
                                                                                                                                                                                 organism="Acyrthosiphon pisum"
|mol_type="mRNA"
|cultivar="developmentstage"
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Aphidiformes;
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REFERENCE AUTHORS ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 15 BJ619443 LOCUS ORIGIN FEATURES COMMENT DEFINITION Query Match
Best Local Similarity
Matches 297; Conserv TITLE source 1242 1182 1122 1002 CGCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGA 1061 526 586 646 297; 466 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 BJ619443 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL189d24 5', mRNA sequence. Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; BJ619443 BJ619443.1 GI:37258203 http://xenopus.nibb.ac. Contact: Tadasu Shin-i Expressed genes in X. laevis embryo Unpublished (2001) Kohara, Y Kitayama,A., Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 707) Xenopus laevis (African clawed frog) Xenopus laevis GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTTGAGAT 1300 GGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCC GGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCC GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT CGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAAATGCGCAAGGGCATGTGTTC CGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTC ACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCT 1121 Conservative Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All partheonemetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)" /tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early /organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="XL189d24" nopus.nibb.ac.jp. location/Qualifiers Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and 22.4%; Score 295.8; DB 8; Pred. No. 2.6e-80; 0; Mismatches 2; is available through the following Length EST 01-OCT-2003 ٥, gastrula 408 1241 1181 647 467 527 587

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                                                                    GTATGGTGTGACATTACCCACTTCAGTACTGTTTATTGCCGGACACGATACTAATCTGGC 989
                                                                                                                           CACCCCGTTATTGGATTTTGATCATTGGCAGCGTTGACGCCCCCATCCACAAAAAACAGGC 929
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Pred. No. 2.2e-65;
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Search completed: June 14, 2006, 14:21:54 Job time : 6948.38 secs

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Result
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290227 seqs, 117694381 residues
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      Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
      GenCore version (c) 1993 - 2006
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                      US-10-449-902-20908
US-11-293-697-2180
US-10-953-349-31412
US-10-953-349-11004
US-11-217-529-79920
US-11-217-529-79920
US-10-449-902-6188
US-10-449-902-13863
US-10-449-902-12516
US-10-449-902-12516
US-10-449-902-151513
US-10-449-902-11476
US-10-449-902-151513
US-10-449-902-151513
US-10-449-902-15256
US-10-449-902-15259
US-10-449-902-1529
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Biocceleration Ltd
Sequence 20908, A
Sequence 2180, Ap
Sequence 34412, A
Sequence 11004, A
Sequence 37, App)
Sequence 37, App)
Sequence 17920, A
Sequence 1786, A
Sequence 1786, A
Sequence 10760, A
Sequence 10760, A
Sequence 10760, A
Sequence 11476, A
Sequence 11476, A
Sequence 27515, A
Sequence 25013, A
Sequence 250, App)
Sequence 2962, Ap
Sequence 2963, Ap
Sequence 13409, A
Sequence 13409, A
Sequence 13409, A
Sequence 80383, A
Sequence 828, App
Sequence 828, App
Sequence 828, App
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US-10-449-902-21495	US-10-449-902-22565	US-10-449-902-25550	US-10-449-902-8467	US-11-217-529-76896	US-10-449-902-741	US-11-246-405-12	US-11-293-697-1224	US-10-449-902-24808	US-10-449-902-25001	US-10-449-902-12853	US-10-449-902-6979	US-10-449-902-18030	US-11-217-529-5697	US-10-449-902-24250	US-11-154-977-36	US-10-449-902-11182	US-11-154-977-42	US-11-154-977-68	US-10-449-902-5189
Sequence 21495, A	Sequence 22565, A	Sequence 25550, A	Sequence 8467, Ap	Sequence 76896, A	Sequence 741, App	Sequence 12, Appl	Seguence 1224, Ap	Sequence 24808, A			Sequence 6979, Ap	Sequence 18030, A	Sequence 5697, Ap	Sequence 24250, A	Sequence 36, Appl	Sequence 11182, A	Sequence 42, Appl	Sequence 68, Appl	Sequence 5189, Ap

ALIGNMENTS

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Sequence 20008, Application US/10449902

Publication No. US20060123505Al

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-0A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: UD 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION DATE: 2002-12-11
NUMBER: DF SEQ ID NOS: 56791
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US-10-449-902-20908/c
                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20908
LENGTH: 1309
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: OTYZA BALÍVA
ORGANISM: OTYZA BALÍVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK071209
DATABASE ENTRY DATE: 2001-12-06
591
                                      332
                                                                                                                             272
                                                                                                                                                                                                                  212
                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                  Similarity
                             TCGACGAGCGTACCCGTAAAACAGGCGAAGCCTTCGCCGCCGGGCTG
                                                                                                                                                                      ĊĠĊAĊĠĊAĠĠŦĠĠĊĠĠĠŦĊĠĊĊĠĀĊĠAĊĠŦĀĠĀĊĊŦŦĠĀĀĠĀĠĊĀĊĊĊĊĠĊĊĠŦĠĠŦŦĠ
ACGAGGCGCATGTCGTGCGACTCGGCGCTCGACGGCGAGCGG
                                                                                  ACGAACTCCTGGAGGACGAGCGCGCGCGCGGAGGAGGACGCCCGTCGCGGCGGTAG
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                                                                                                                                                                                                                  CGCGNGGTGGTGAGCTAATCGCCTATCTCGGACATTACCAACGCCAGCGTCTGGTAGCCG
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nilarity 51.5%;
Conservative
                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                           Score 38; DB 6; Length 1309;
Pred. No. 0.0051;
0; Mismatches 81; Indels
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545
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                                                                                    592
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RESULT 2 US-11-293-697-2180/c ; Sequence 2180, Application US/11293697

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; Publication No. US20060105376A1
; GEMERAL INFORMATION:
; APPLICANT: HELLX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVE1 full length cDNA
FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PAtentin Ver. 2.1
; SEQ ID NO 2180
; LENGTH: 2879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2180
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; ORGANISM: Zea mays subsp. mays
US-10-953-349-34412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34412, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.3
SEQ ID NO 34412
LENGTH: 979
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 7750-1579pUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                       649
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529
                                      343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 GCATGGTGTGGCGGAAGTCGCCCAGCGGGGCGCTGATCATCTCGGCCGTGAGGTCCGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83; Conservative
                                                                                                                                                                                                                                                                            163 ACCCCAGACGCATGGCCAACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 AACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTCGGACATTACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 CCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCAACCTGGCCGGTAA 193
                                                                                                                                                                                                                                                                                                                     95;
                                                                                                        GCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCT 295
GTCGGTGAGAGAGGCG 514
                                      ACCCGTAAAACAGGCG 358
                                                                             GCGGGCGAGGCAGTCGCGGGACCGCGTGCACGACCGGTAGAGGCTGAGCACGGCGAGCCA
                                                                                                                                                         GAGCCGATCGACGAGACGGGCCTTCGCCGGCGGCGGAGCGCGGGGGGCGCAGCGGCGT 590
                                                                                                                                                                                              GAGCTAATCGCCTATCTCGGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTG
                                                                                                                                                                                                                                     ACACCCGGCGAAGGACCGGGAGCACCGGGACACGCGGACCTGGCTCACTGGTGAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAACGGCGCTTGGAGTGCACCGAGCTGGACACCAGTTGCT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCGGCCTTGCTATTGAGGAAGGAGGTGTCCCCAAAGGCGTCTCCGGCCCGGCCAACGT
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.7%;
                                                                                                                                                                                                                                                                                                                                   2.6%;
                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.2; DB 7; Length 2879; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                     Score 35; DB 6; Length 979; Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                   Mismatches 101;
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                                                                                                                                                                                                                                                                                                                   Indels
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US-10-953-349-11004/c
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 79920
LENGTH: 1257
TYPE: NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 79920, Application US/11217529

Publication No. US20060099612A1

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INCENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11004, Application US/10953349
publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.3 SEQ ID NO 11004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                     Matches
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579FUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: S-38-285
                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2271
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 2.5%;
Local Similarity 60.4%;
                                                                                                                                                                   Local Similarity
mes 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1674 CCTGCGAAAACTAGTTTGCTCTTTGATCTTT 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1272 AGCAÇGCATACCGGCGTGCAGTTTGAGATCT 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1734 TGAACCGGGACATGTTCGGGTGATATGTACCTGAGAAGGGTTTCTGCAGATCTTGAAGGA 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1212 TGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAATCGTGAATGA 1271
                                                                                                                          671 CCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTC 730
193
                                       731 TCCTGCAACAAGCACAGG 748
                                                                                CCGAGTCTGTCTCAAAAATGGGTTTGGTGAGCGTGCCATCAGCGCTGAAGGAGCCGTATT
  TCATCCAATCCGTAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                     Conservative
                                                                                                                                                                                2.5%;
  176
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                                                                                                                                                                 Score 33.2; DB Pred. No. 0.24; 0; Mismatches
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Pred. No. 0.3;
0; Mismatches
                                                                                                                                                                                                          DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
                                                                                                                                                                     28;
                                                                                                                                                                                                          Length 1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 6 US-11-293-654-37

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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
COUNTRIES DEFENCE VAN 9 9
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APPLICANT: Taraporewala, Zenobia F.

TITLE OF INVENTION. ANTIGEN DELIVERY PLATFORM

FILE REFERENCE: 4239-69406-02

CURRENT APPLICATION NUMBER: US/11/293,654

CURRENT FILING DATE: 2005-12-02

PRIOR APPLICATION NUMBER: US 60/633,036

PRIOR FILING DATE: 2004-12-03

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin version 3.3

SEQ ID NO 37

LENGTH: 3431
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Best Local Similarity
Matches 46; Conserv
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SEQ ID NO 8987
LENGTH: 1396
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APPLICANT: The Government of the United States of America, as
APPLICANT: Represented by the Secretary of the Dept. of Health and Human
APPLICANT: Services
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Publication No. US20060122368A1
                                                                                                                                                                                                                                                                                                                                             -10-449-902-8987
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK106335
DATABASE ENTRY DATE: 2002-08-28
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lon No. US20060123505A1
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                                                                                                                                                                                                         Score 32;
Pred. No.
                                                                                                                                                                                                         DB 6; Length 1396; 0.68;
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                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A020591-US
                                                                              SOFTWARE: PatentIn Ver. SEQ ID NO 17204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17204, Application US/10449902 Publication No. US20060123505A1
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LENGTH: 1489
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                                                                                                                        CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK104957
DATABASE ENTRY DATE: 2002-08-28
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APPLICANT: Bio-oriented Technology Research Advancement Institute APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205YI-US
FULL REPERENCE: MOA-A0205YI-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR ETILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
ORGANISM: Oryza sativa
                                                  ENGTH: 1600
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les 70; Conserv
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US-10-449-902-13863/c
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RESULT 11
US-10-449-902-12516/c
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SEQ ID NO 1363
LENGTH: 3129
TYPE: DNA
ORGANISM: Oryza sativa
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Best Local :
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
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DATABASE ACCESSION NUMBER: AK067664
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
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DATABASE ACCESSION NUMBER: AK111211
DATABASE ENTRY DATE: 2001-12-06
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                                                                                                                                                                       GGTGAACCCGGAGATGTTGGAGAGCATGGAGGAGGAACGGCCGCGCCATTGCGGAGGGA 2763
                                                                                                                                                                                                    GCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCC 1178
                                                                                   ACCAGGAGTGCTG 2750
                                                                                                                             GCCCGGAGAGGTG 1191
                                                                                                                                                                                                                                                           TGCGTGGAACGGGTTACCGAGTTGGAAGCCAGAGGGTGAGTGCGGCTCGTCGAAGCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%;
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; Pred. No. 1;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31.4; Di
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 101;
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RESULT 12
US-10-449-902-10760/c
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US-10-449-902-10760
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Publication No. US20060123505A1
GENERAL INFORMATION:
                    SEQ ID NO 10760
LENGTH: 1344
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION UNBER: AK108108
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12516, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
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SEQ ID NO 12516
LENGTH: 2144
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                                                                                                                                                                                                                                       APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Poundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UF 10/449,902
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-39
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER: OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: OTYZA SATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK109864
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1532 GTCCACCCACGTCTCGTTGTTGCCGGAGCCGCCGGCGGCGGCGGCGGCGTCCCAGC 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1592 GTTGTAGTGGTTCGCCGCGATCGCCACCTTCTTCTTCCTCAGCTTCCGCCTTGCGGACGAA 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1652 CGGCGGGGTGGGCAGCCAGCTGGCTCAGCCGGAGGTACTCCATCCCCTTCTTCTCGCGCG 1593
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Pred. No. 1.7;
0; Mismatches
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Query Match

Best Local Similarity

2.3%;

Score 31; Pred. No.

DB 1.5;

6

Length 1344;

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1107 GGGGTGGGGCCGTGGGGGGGTGAGTGACAACAGCTACAAGTCACTATTCAGTGCTCCCCGG 1048

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Sequence 27515, Application US/10953349
Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27515
LENGTH: 1393
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; TITLE OF INVENTION: NOVel full length cDNA; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 707
; LENGTH: 2791
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US-11-293-697-707
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US-11-293-697-707/c
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                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
Matches 61; Conserv
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663 GGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCCATCAATGCTGACGGA 722
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                                                           TAACCTTTAGGTACATCTTGCAGGTTCTACCAACAGGTAAGCTTAACAGCTGACAGTCCA
                                                                                              ТАЛАССТСЯДАЛАСАСВАССВАЛАССТСТТСАТТАЛССДОСАСТАССАТССВАЛСТСАЛ 662
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                                                                                                                                         Conservative
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ilarity 55.0%;
Conservative
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                                                                                                                                                           2.3%;
                                                                                                                                     Score 30.8; DI
Pred. No. 1.8;
0; Mismatches
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Search completed: June 14, Job time: 41.2281 secs
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SEQ ID NO 11476
LENGTH: 1461
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108824
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-12-11
PRIOR PILING DATE: 2002-13-11
NUMBER: OF SEQ ID NOS: 56791
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                           1072
                                                                                                                                                          1012 CACGCCGATCTTGCTCATGTTGACGAAGGAGACGATGAAGTCGGCGAAGAACTCGTCGTC
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                                                                                                                    373
                                                                                                                                                                                               313 GTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAAGCCTTCGCCGCC 372
                                                                                                                                                                                                                                                                             253 CGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCGCAGTCTGGTCAG 312
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                                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                  GG 374
                                                                                                                                                                                                                                       CGGCGACGGCGGGTTGACAGCAGAGCACTTGTGCCTGATCTCGCCGTGGGAGTGGGTGAG
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ilarity 53.3%;
Conservative
                  2006, 14:23:15
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Pred. No. 1.
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                1322
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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10064.996 Million cell updates/sec
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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             0 US-10-933-115-1

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US-10-15-660-3

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4 US-11-056-354-3

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US-10-282-122A-7167

US-09-866-379-5

US-09-866-379-5

US-10-933-115-5
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US-09-866-379-1

US-10-034-985-1

US-10-430-356-1

US-10-601-319-1
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     Sequence 1, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
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12.4	12.4	12.4	12.4	15.1	15.6	16.3	16.6	16.9	29.5	29.5	30.2	30.2	50.4	50.4	52.1	55.1	94.7	94.7	94.9	95.5	95.6	95.6	95.7	95.7	95.7	97.0	97.0
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ALIGNMENTS

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US-09-777-566A-1
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CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
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US-09-777-566A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-6
FILE REFERENCE: DIVER1370-6
Query Match
Best Local Similarity
Matches 1323; Conserv
                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09777566A Patent No. US20010055788A1 GENERAL INFORMATION:
                                                                                                           ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1320)
NAME/KEY: misc feature
LOCATION: (1)..(1323)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                    TYPE: DNA
100.0%; Score 1322; 
llarity 100.0%; Pred. No. 0; 
Conservative 0; Mismatches
                                              DB 3;
  0,
                                            Length 1323;
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CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                                                                                                        TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG
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APPLICANT: BARKEYN, STELLON,
APPLICANT: O'DONOGHUE, Bileen
ITITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERNI370-7
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR REPLING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR PRILING DATE: 1999-03-01
PRIOR PRILING DATE: 1999-03-01
PRIOR PRILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 10
LENGTH: 1323
TYPR: DNA
                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n is
; NAME/KEY: CDS
; LOCATION: (1)...(1323)
; OTHER INFORMATION:
US-09-866-379-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Kevin
APPLICANT: BARTON, Nelson
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US-09-866-379-1
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                                                             TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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                                                                     CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGAGGTGAAACTGACC
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                                                       CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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Sequence 1, Application US/10034985
Publication No. US20030049815A1
GENERAL INFORMATION:
APPLICANT: K-etz, Keith
FILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT PILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/99/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1997-03-01
PRIOR FILING DATE: 1997-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFOR
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Best Local Similarity 100.0%;
Matches 1323; Conservative 0
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NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or
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TYPE: DNA
ORGANISM: Escherichia
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GCCTTCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                                                 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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Pred. No. 0;
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RESULT 4
US-10-430-356-1
US-10-430-356-1
; Sequence 1, Application US/10430356
; Publication No. US20030232041A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
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CURRENT APPLICATION NUMBER: US/10/430,356
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR APPLICATION NUMBER: US/09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-03-01
VUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
VUMBER: 0F SEQ ID NOS: 4
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NAME KEY: CDS
LOCATION: (1)...(1320)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Matchur, Eric J.
APPLICANT: Matchur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND TITLE OF INVENTION: AND USING THEM FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-601-319-1
                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10601319 Publication No. US20040091968A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
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Matches 1323; Conservative C
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TYPE: DNA
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NAME/KEY: CDS
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TOCATTON: 016
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, Nelson Robert
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT PILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
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Publication No. US20050281792A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/910,79
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1323
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                                                                                                                              CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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US-09-866-379-7

US-09-866-379-7

Sequence 7, Application US/09866379

Patent No. US2020136754A1

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GARETT, James
APPLICANT: O'DONOGHUE, Sileen
APPLICANT: O'DONOGHUE, Sileen
APPLICANT: O'DONOGHUE, SILOEN
CURRENT FILING DATE: 1001-05-24
PRIOR APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR PPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/299,214
PRIOR APPLICATION NUMBER: US 09/259,214
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1901)
; OTHER INFORMATION: n is any nucleotide
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Best Local Similarity 99.4
Matches 1293; Conservative
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        TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG
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                                                                                                                                                     GATTCACACCAGTGGAACACCTTGCTAAGTTTTGCATAACGCGCAATTTTATTTGCTACAA
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Query Match 97.4%; Score 1287.8; DB 6; Length 1901; Best Local Similarity 99.5%; Pred. No. 0;	S	FEATURE: NAME/KEY: LOCATION: FEATURE:	SEQ ID NO 3 LENGTH: 1901 TYPE: DNA ORGANISM: Escherichia coli	PRIOR PRIOR NUMBER SOFTWA	; PRIOR APPLICATION NUMBER: US 09/291,931 ; PRIOR FILING DATE: 1999-04-13 ; PRIOR FILING DATE: 09/259,214 ; PRIOR FILING DATE: 1999-03-01	; PRIOR APPLICATION NUMBER: US 09/580,515 ; PRIOR FILING DATE: 2000-05-25 ; PRIOR PILING DATE: 1999-05-25 ; PRIOR FILING DATE: 1999-05-25	; CURRENT APPLICATION NUMBER: US/10/156,660 ; CURRENT FILING DATE: 2007-10-01 ; PRIOR APPLICATION NUMBER: US 09/866,379 ; PRIOR FILING DATE: 2001-05-24	APPLICANT: Mathur, Eric J. TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM FILE REFERENCE: 09010-029007	APPLICANT: Gray, Kevin A. APPLICANT: Barton, Nelson R. APPLICANT: Garrett, James B. APPLICANT: O'Donoghue, Elleen	; Publication No. US20030103958A1 ; GENERAL INFORMATION: ; APPLICANT: Short, Jay M. ; APPLICANT: Kretz, Keith	RESULT 8 US-10-156-660-3 ; Sequence 3, Application US/10156660	OY 1261 ATCGTGAATGAAGCACGCATACCGGGGTGCAGTTTGAGAT 1300	QY 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	Db 1328 CAGATGCGTGATAAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1387	1081 CGTCGGCTAAGCGATTAACAGCCAGTGGATTCAGGTTTCCAGACTTTACAG		Db 1148 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGACCTCAACTGG 1020	1088 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 114
da	р Q	da da	QQ VQ	עץ מם	da Qy	da Qy	dg Qy	Qy dd	Qy	Db Qy	ДУ	Qy db	Db Qy	D S	S & &	Q _V	Db	Matches
1021 AUGUTTUU GASTUMAU UU GASTAMA KAUGUU LAAGSTEGTISAMATIKA 1021 TIGAA (GETIGE 1208 AUGUTTUU GASTAMA CAUGUU GASTAMA CAUGUU GAGAA CTAGAA CTAGAA CAUGUU GAAA CTAGAA CAUGUU GAAA CTAGAA CAUGUU GAAA CTAGAA CAUGUU GAAA CAUGUU GAAA CTAGAA CAUGUU GAAA CAUGUU GAAAA CAUGUU GAAA CAUGUU GAAAA CAUGUU GAAAAA AAAAAAAAAA				781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCCGGGTGGGGAAGGATCACC	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGIIIIIIIIII	601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTG 		421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGC 	361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGGGTACCCGTAAAACAGGCGAA 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG	368 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC		61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTCGTGATTGTCAGTCGTCATGGT	1 ATGARAGGATCTTRATCCCATTTTRATCTCTTCTGATTCCGTTRACCCCGCARTCTGCA	

Query Match 97.4%; Score 1287.8; DB 8; Length 1901; Best Local Similarity 99.5%; Pred. No. 0; Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0; Qy 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	; NAME/KEY: misc_feature ; LOCATION: 403 ; OTHER INFORMATION: n = A,T,C or G US-10-601-319-7	FEATURE: NAME/KEY: CDS LOCATION: (188)(1483) FEATURE:	AL AL Das	; PRIOR APPLICATION NUMBER: US 08/910,798 ; PRIOR FILLING DATE: 1997-08-13 ; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: FastSED for Windows Version 4.0	PRI PRI PRI	PRI PRI PRI	PRICUR	Mathur, Eric NVENTION: RECON NVENTION: AND NVENTION: AND	o g B g	; Publication No. US20040091968A1 ; GENERAL INFORMATION: ; APPLICANT: Short, Jay M. ; APPLICANT: Kretz, Keith A.	RESULT 9 US-10-601-319-7 ; Sequence 7, Application US/10601319	Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	QY 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200	Qy 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140
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1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGACCTGGTGTTTGAACGCTGG 1080	961 TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCGCACTGGAGCTCAACTGG 1020 	901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960 	841 CGCACGCCAGAGGTTGCCCCGCAGCCGCCCACCCCGTTATTGGATTTGATCATGGCAGCG 900	781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840 	721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780	661 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	601 CTTAAACGTGAGAAACAGGACGAAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	541 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600 	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480 	361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAAGGCAGATACG 420 	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGAGGGTACCCGTAAAACAGGCGAA 360 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 300 	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180

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LENGTH: 1901

TYPE: DNA
ORGANISM: Escherichia coli
PEATURE:
NAME/KEY: CDS
LOCATION: (188)...(1483)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 403
COTHER INFORMATION: n = A,T,C or
US-10-933-115-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: Mathar, Eric J.
APPLICANT: Mathar, Eric J.
APPLICANT: Mathar, Eric J.
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US/09/318,528
PRIOR APPLICATION NUMBER: US/09/318,528
PRIOR APPLICATION NUMBER: US/09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR SOUTHARE: PASTSEQ for Windows Version 4.0
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Publication No. US20050281792A1
GENERAL INFORMATION:
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Best Local Similarity 99.5%;
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                                   ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                                               | CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260
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Sequence 3. Application US/11056354

Publication No. US20050246780A1

GENERAL INFORMATION:

APPLICANT: ESHORT, Jay M.

APPLICANT: KRETZ, Keith

APPLICANT: KRETZ, Keith

APPLICANT: GARY, Kevin A.

APPLICANT: GARRETT, James B.

APPLICANT: O'DONOCHUE, Eileen

APPLICANT: O'DONOCHUE, Eileen

APPLICANT: MATHUR, Eric J.

TITLE OF INVENTION: POR MAKING AND USING THEM FILE REFERENCE: 564462001803/D1370-9C1

CURRENT APPLICATION NUMBER: US/11/056,354

CURRENT APPLICATION NUMBER: US 10/156,660

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/80,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR PRI
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US-11-056-354-3
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Best Local Similarity
Matches 1293; Conserv
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LOCATION: (403)..(403)
OTHER INFORMATION: n is any
-11-056-354-3
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TYPE: DNA
ORGANISM: Escherichia
FEATURE:
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; Sequence 7167, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
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US-10-282-122A-7167
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APPLICANT: FORSYTH, R.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITEA.034A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7167
LENGTH: 1299
TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.4%;
Best Local Similarity 99.5%;
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OR FILING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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Carr, Grant
Carr, Grant
Robert
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      TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                            GCCTTCGCCGGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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Forsyth, R.
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Pred. No. 0;
0; Mismatches
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US-09-866-379-5
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Sequence 5, Application US/09866379
Patent No. US20020136754A1
GEMERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: PATENTIN PATENTING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: PATENTIN PATENTING DATE: 1997-08-13
LENGTH: 1901
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Best Local Sim:
Matches 1292;
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ORGANISM: Escherichia coli
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1901)
OTHER INFORMATION: n is any nucleotide
-09-866-379-5
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                                            CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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                                                                                                                                                                                                             AACGTGACTGACGCGATCCTCAGCAGGGCGCAGGAGGGTCAATTGCTGACTTTTACCGGGCAT
                                                                                                                                                                                                                                                                  TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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                     CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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Pred. No. 0;
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        Sequence 9, Application US/09866379

Sequence 9, Application US/09866379

Patent No. US20020136754A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: SHORT, Jay

APPLICANT: BARTON, Nelson

APPLICANT: BARTON, Nelson

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

ITILE OF INVENTION: RECOMBLINANT BACTERIAL PHYTASES AND

FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT PILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 08/259,214

PRIOR APPLICATION NUMBER: US 08/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOFTWARDER: DATE: 1997-08-13
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FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity 99.4%;
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Pred. No. 0;
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GENERAL INFORMATION: Verti A.

APPLICANT: Short, Jay M.

APPLICANT: Short, Keyin A.

APPLICANT: Gray, Keyin A.

APPLICANT: Barton, Nelson Robert

APPLICANT: Barton, Nelson Robert

APPLICANT: Gray, Keyin A.

APPLICANT: Barton, Nelson Robert

APPLICANT: Mathur, Eric J.

ITILE OF INVENTION: AECOMBIANT PHYTASES AND METHODS OF MAKING

ITILE OF INVENTION: AND USING THEM

FILE REFERENCE: 09010-029011

CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/80,515

PRIOR APPLICATION NUMBER: US 09/80,515

PRIOR APPLICATION NUMBER: US 09/50,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/290,214

PRIOR APPLICATION NUMBER: US 09/290,798

PRIOR APPLICATION NUMBER: US 09/290,214

PRIOR APPLICATION NUMBER: US 09/290,210

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5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

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9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

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10: /EMC_Celerra_SIDS3/ptodata/2/ina/BCCMB.seq:*
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ALIGNMENTS

US-09-259-214-1

(Sequence 1, Application US/09259214A)

Fatent No. 6110719

(GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVER1370-1

(CURRENT APPLICATION NUMBER: US/09/259,214A)

(CURRENT FILING DATE: 1999-03-01

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 4

SOPTWARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1323

TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: cDS
LOCATION: (1)...(1320)

NAME/KEY: CDS
LOCATION: (1)...(1323)

OTHER INFORMATION: n = A,T,C or G

Query Match 100.0%; Score 1322; Best Local Similarity 100.0%; Pred. No. 0; Matches 1323; Conservative 0; Mismatches 181 181 121 121 61 13 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA Mismatches DB 3; 0; Length 1323; Indels 0, Gaps 180 240 180 120 120 240 60 0,

301 241

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CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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                                                       ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTTGAGATCTCATCACCATCACCATCAC
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; ORGANISM: Escherichia co;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; NAME/KEY: misc feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A.
US-09-318-528-1
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Patent No. 6183740
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION NUMBER: US/09/318,528
CURRENT APPLICATION NUMBER: 09/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 09/210,798
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER: FEATURE DATE: 1999-03-01
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Best Local Similarity
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                      AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                  TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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Pred. No. 0;
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Sequence 1, Application US/09291931A

Patent No. 6190897

GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003

CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1999-04-13

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER FILING DATE: 1997-08-13

EARLIER APPLICATION NUMBER: 09/259,214

EARLIER FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 4
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SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or G
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Query Match 100.0%; Score 1322; DB 3; Length 132: Best Local Similarity 100.0%; Pred. No. 0; Matches 1323; Conservative 0; Mismatches 0; Indels	ORGANISM: Escherichia coli ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)(1320) ; NAME/KEY: misc feature ; LOCATION: (1)(1323) ; OTHER INFORMATION: n = A,T,C or G US-09-580-515-1	PRIOR PRIOR PRIOR NUMBEI SOFTWI SEQ ID LENGT	; FILE REFERENCE: 09010/029003 ; CURRENT APPLICATION NUMBER: US/09/580,515 ; CURRENT FILING DATE: 1999-05-25 ; PRIOR APPLICATION NUMBER: 09/318,528 ; PRIOR FILING DATE: 1999-05-25 ; PRIOR FILING DATE: 1999-05-25 ; PRIOR FILING DATE: 1999-04-13 ; PRIOR APPLICATION NUMBER: 08/910,798	RESULT 4 US-09-580-515-1 ; Sequence 1, Application US/09580515 ; Patent No. 6720014 ; GENERAL INFORMATION: ; APPLICANT: Kretz, Keith ; TITLE OF INVENTION: NOVEL PHYTASE	Qy 1321 TAA 1323 	Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCACCATCACCATCAC 	Qy 1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA	Qy 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGAGGTGAAACTGACC	Qy 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG	Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGATGAACTGGTGTTTGAACGCTGG	Oy 961 TITATIGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCGCACTGGAGCTCAACTGG	Qy 901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG	Qy 841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG
0; Gaps 0; Oy	QY QY Db	4d 4d 4d 4d	25 SA BA	OY OY OH	Qy da	ACCATCAC 1320 OY ACCATCAC 1320 Db	TTACGCAA 1260 QY Db	AACTGACC 1200 QY AACTGACC 1200 Db	ACTTTACAG 1140	AACGCTGG 1080 Qy AACGCTGG 1080 Db	TCAACTGG 1020 OY	CAGTACTG 960 CY CAGTACTG 960 Db	ATGGCAGCG 900 QY ATGGCAGCG 900 Db
1021 ACGCTTCCCGGTCAACAACAGCCGCCAGGTGGTGAACCTGGTGTTTTAACAGCTGGTGGTGAACCTGGTGTTTCCAGACGTTGGTGTGAACGCTGGTGTTTCAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTGGTGAACGCTTGAACAGCTAACAGGTAACAAGGCAAGTGGAATTCAAGGTTTCGCTGGTTGTTCCAAGACTTTACAGGTAACAGGTAACAAGGCAAGTGGAATTCAAGGTTTCAAGGTTTTCCAAGACTTTAACAAGGTAACAAGGTAACAAGGTAACAAGGTAACAAGGTAACAAGGTAACAAGGTAACAAGAACAAGAACAAGAACAAAAAAAA	O1 TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG	781 GATTCACCAGIGGAACACCTTGCIAAGTTTGCATAACGGCAATTTTATTTGCTACAA 840	AAGGTCAGCCGCACAATGTCTCATTAACCGGTGCGGTAAGCCTGCCATCAATGCTGACCAATGATCACTGACCAATGATCACCGGTGCGGTAAGCCTGACCATCAATGCTGACCATCAATGCTGACCATCAATGCTGACCGAGGTAAGCCTCGCCATCAATGCTGACCGAGGTTAAGCCGCGGGGTAAGCCTCGCCATCAATGCTGACCCGAGGAATGACCACAGGGAATGCCGGAGCCCGGGGTGGGGAAGGATCACCCGAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCCGGGGTGGGGAAGGATCACCCGAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCCGGGGTGGGGAAGGATCACCCGAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCCGGGGGTGGGGAAAGGATCACCCGAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCCGGGGGTGGGGAAAGGATCACCC	CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAACTTGTGC	481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	421 TCCAGTCCCGATCCGTTATTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480	361 GCCTTCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 360 	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 300	181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60

Query Match Best Local Similarity 100.0%; Score 1322; DB 3; Length 1323; Best Local Similarity 100.0%; Pred. No. 0; Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGARAGCGATCTTARTCCCATTTTTATCTCTTCTGATTCCGTTRACCCCGCAATCTGCA 60	; NAME/KEY: misc_feature ; LOCATION: (1)(1323) ; OTHER IMPORMATION: n is any nucleotide ; NAME/KEY: CDS ; LOCATION: (1)(1323) ; OTHER INFORMATION: US-09-866-379-1	; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 1 ; LENGTH: 1323 ; TYPE: DNA ; ORGANISM: Escherichia coli	PRIOR APPLICATION NUMBER: US 09/291,931 PRIOR PILLING DATE: 1999-04-13 PRIOR APPLICATION NUMBER: US 09/259,214 PRIOR APPLICATION NUMBER: US 08/910,798 PRIOR APPLICATION NUMBER: US 08/910,798 PRIOR FILING DATE: 1997-08-13		APPLICANT: O'DONOGHUE, Bileen TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF FILE REFERENCE: DIVER1370-7 CURRENT BYTICATION NUMBER: US/09/866,379	APPLICANT: DIVERSA CORPORATION APPLICANT: SHORT, Jay APPLICANT: KRETZ, Keith APPLICANT: GRAY, Kevin APPLICANT: GRAYN, Melson APPLICANT: GARRETT, James	RESULT 5 US-09-866-379-1 ; Sequence 1, Application US/09866379 ; Patent No. 6855365 ; CENERAL TUROPHARTON.	1321 TAA			111 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC	1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
OY 1021 AGGETTCCCGGTCAGCCGGCAGGTGAACTGGTGTTTAAACGCCTGGTOTTCGAACTGCTGGTTTTAAACGCTGGTGTTTAAACGCTTGGTGTTTTAAACGCTTGGTGTTTTAAACGCTTGGTGTTTAAACGCTTGGTGTTTTAAACGCTTGGTGTTTTAAACGCTTGGTCAGACTTTACAGGTTAACACGCCAGAGTTCAGGTTTCAGACTTTTACAGGTTAACAGCTTTACAGGTTAACAGCTAGACTTTAAAACAGCCAGTTGAATTCAGGTTTCAGAGTTTCAGACTTTAAAACAGCTAAACAGCCAGTGAATTCAGGTTCAGAGTTTCAGAGTTTAAAACTGACCTTAAAACAGCCAGTTGAAAACAGCCCGCTGGTCATTAAATACGCCCGCC	901 TYGACGCCCATCCACCGCAAAACAGGCGTATGGTCTGACATTACCCACTTCAGTACTG	GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG	OY 721 GAGATATITCTCCTGCAACAAGCACAGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780	7 7	OY 601 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660	481 AACGTGACCGCGATCCTCAGCAGGGCAGGGTCAATTGCTGACTTTACCGGGCAT 481 AACGTGACCGCGATCCTCAGCAGGGCAGGGTCAATTGCTGACTTTACCGGCAT 481 CGCCAACCGCGATCCTCAGCAGGGAGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 541 CGCCAACCGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 541 CGCCAACCGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 541 CGCCAACCGGCGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 541 CGCCAACCGGCGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 541 CGCCAACCGGCGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 541 CGCCAACCGGCGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTTGTGC 541 CGCCAACCGGCGTTTCGCCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTTGTGCAAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAACTTTGTGCAAACTTTGTGCAAACTTTGTGCAACTTTGTGCAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGTGAACTTTGAACTTTGTGAACTTTGAACTTTGTGAACTTTGTGAACTTTGAACTTTGTGAACTTTAACTTTTAAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAACTTTGAAACTTTGAAAAAAAA	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTCGCCGTTTGCCAACTGGATAACGCG	Qy 361 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420	Qy 301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA 360	QY 241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 300	QY 181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGGGTGAGCTAATCGCCTATCTC 240	Qy 121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180

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LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1901)
OTHER INFORMATION: n is any nucleotide
US-09-866-379-7
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APPLICANT: GARRION, Netson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
ITILE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
COMPMENDE: Dataset of Sec ID NOS: 10
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GENERAL INFORMATION;
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
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   GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG
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    Application US/09866379
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APPLICANT: GARRET, NOTALL APPLICANT: BARTON, NOISON
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OP INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
PILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
PRATTIRE:
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NAME/KEY: misc_feature

LOCATION: (1)...(1901)

OTHER INFORMATION: n is any nucleotide
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Kevin
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Best Local Similarity
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Sequence 9, Application US/09866379

PARENT NO. 685365

GENERAL INFORMATION

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: SHORT, Jay

APPLICANT: BARTON, Nelson

APPLICANT: BARTON, Nelson

APPLICANT: GARRETT, James

APPLICANT: O'DONOGHUE, Bileen

71TLE OF INVENTION: RECOMBLMANT BACTERIAL PHYTASES AND USES THEREOF

FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT PILLING DATE: 2001-05-24

PRIOR APPLICATION DATE: 2000-05-25
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PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 9
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Best Local Similarity 99.4%;
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NAME/KEY: misc_feature
LOCATION: (1). (1901)
OTHER INFORMATION: n is any nucleotide
-09-866-379-9
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TYPE: DNA
ORGANISM: Escherichia coli
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 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                                                            APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GARRETT, James
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US-09-866-379-6
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TYPE: DNA ORGANISM: Escherichia coli FEATURE:
                                                  LENGTH: 1901
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Best Local Similarity
Matches 1290; Conserv
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                                                                                                           GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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CAGCCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA
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Sequence 9, Application US/09540149A

Patent No. 6511699

GENERAL INFORMATION:

APPLICANT: Lei, Xingen

IIILE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY

FILE REFERENCE: 19603/2791

CURRENT APPLICATION NUMBER: US/09/540,149A

CURRENT FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 60/127,032

PRIOR APPLICATION WIMBER: 60/127,032

PRIOR FILING DATE: 1999-03-31

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 9

LENGTH: 1489

TYPE: DNA

ORGANISM: Becherichia coli
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Best Local Similarity 97.9%;
Matches 1280; Conservative
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CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA
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RESULT 11
US-10-266-041A-9
; Sequence 9, Application US/10266041A
; Patent No. 6974690
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVED
; FILE REFERENCE: 19603/2798
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CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN NOS: 9
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 9
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                GATTCACACCAGTGGAACACCTTGCTAAGTTTTGCATAACGCGCAATTTTTATTTTGCTACAA
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8 9 9 9 9 Q	Query Best 1 Match Qy	(O)	GENER APPL TITL FILE CURR CURR PRION	RESULT 12 US-09-715-477- ; Sequence 2,	B &	P 9	g Qy	B 8	B &	유 왕	음 성	å ð
	Query Match 95.5%; Score 1263; DB 3; Length 1486; Best Local Similarity 98.4%; Pred. No. 0; Matches 1275; Conservative 0; Mismatches 21; Indels 0; Gaps 0; 1 ATGANAGCGATCTTAATCCCATTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.1 EQ ID NO 2 LENGTH: 1486 TYPE: DNA ORGANISM: Escherichia coli 09-715-477-2	GENERAL INFORMATION: APPLICANT: Lei, Xingen TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE TITLE REFERENCE: 1960;4031 FULB REFERENCE: 1960;4031 CURRENT APPLICATION NUMBER: US/09/715,477 CURRENT FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/166,179	12 15-477-2 nce 2, Application US/09715477	1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATCAC 1308	1201 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260 	1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200 	1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140 	1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080 	961 TITATIGCCGGACACGATACTAAICTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020 	901 TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960 	841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTGGATTTGATCATGGCAGCG 900
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APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENES
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR APPLICATION NUMBER: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
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US-09-715-477-4
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Best Local Similarity
Matches 1268; Conserv
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TYPE: DNA
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                AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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ATCGTGAATGAAGCGCGCATACCGGCGTGCAGTTTG
                                                         CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCCGGTTTTTACGCAA
                                                                         CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                                  CAGATGCGTGATAAAACGCCGCTATCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                                                    CAGATGCGTGATAAAACGCCCGCTGTCATTAAATACGCCGCCCCGGAGAGGGTGAAACTGACC
                                                                                                                                                                         CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG
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US-08-910-798-1

Sequence 1. Application US/08910798

Fatent No. 5876997

GENERAL INFORMATION:

APPLICANT: KRETZ

ITILE OF INVENTION: NOVEL PHYTASE

TITLE OF INVENTION: NOVEL PHYTASE

TITLE OF INVENTION: NOVEL PHYTASE

INUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: California

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION NUMBER: US/08/910,798

FILING DATE: August 13,1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 38,347

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/029001

TELECOMMUNICATION INFORMATION:

TELEPAN: 619/678-5099

INFORMATION FOR SEQ ID NO: 1:

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; FEATURE:
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; LOCATION:
US-08-910-798-1
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Best Local Similarity 96.1%;
Matches 1272; Conservative
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LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
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                                                         GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                                                                                        AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                                   CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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RESULT 15
US-09-489-039A-341
US-09-489-039A-341
Sequence 341, Application US/09489039A
Patent No. 6610836
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
FITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 341
LENGTH: 1266
                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-341
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                       GGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTCGGACATTACCAACGCCAGCGTC
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llarity 48.7%;
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Pred. No. 1.7e-10;
0; Mismatches 210;
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Job time : 269.494 secs

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35.44.6
36.66.66.88
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length: 2000000000
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Match
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1. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*

4. /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

5. /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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7741.348 Million cell updates/sec
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   atgaaagcgatcttaatccc.....gcagtttgagatctcatcta 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
   GenCore version (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB
     0000010000100001000001
US-10-449-902-6979
US-11-293-697-2180
US-11-293-697-2180
US-10-953-349-11004
US-10-953-349-27515
US-10-449-902-13863
US-10-449-902-15013
US-11-293-697-707
US-10-449-902-15013
US-10-449-902-1503
US-10-449-902-12803
US-10-449-902-12803
US-10-449-902-12803
US-10-449-902-12803
US-10-449-902-12803
US-10-449-902-25657
US-11-217-529-80383
US-10-449-902-2911
US-10-449-902-2911
US-10-449-902-2911
US-10-449-902-2966
US-10-449-902-2966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.1.9
Biocceleration
sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
79979, Ap
79979, Ap
2180, Ap
211004, A
8987, Ap
13868, A
13868, A
13868, A
15760, A
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Que Bees Antr Qy Db Oy Db Db	RESUL US-10	
Query Match 2.9%; Score 37.6; DB 6; Length Best Local Similarity 50.6%; Pred. No. 0.0073; Best Local Similarity 50.6%; Pred. No. 0.0073; Matches 91; Conservative 0; Mismatches 89; Indels 115 CATGGTGGGTGCTCCAACCAACGCCACCCAACTGATGCAGGATGT 645 CATCTTGCAGACGGTCGACCTCAACGAACCGCACCAGTCGAAGGTCGT 175 TGGCCAACCTGGGCGGTAAAACTGGGAGACTGACACCGCGCGCG	ISULT 1 -:10-449-902-6979/c -:10-449-902-6979/c -:10-449-902-6979/c -:10-449-902-6979/c -:10-449-902-6979/c -:10-449-902-6979/c -:10-449-902-6979/c -:10-449-902-6979 -:10-449-902-6979	29.4 2.2 364 7 US-11-154-977-74 29.4 2.2 702 6 US-10-449-902-5189 29.4 2.2 807 7 US-11-154-977-68 29.4 2.2 1161 7 US-11-154-977-42 29.4 2.2 1161 7 US-11-154-977-36 29.4 2.2 1161 7 US-11-154-977-36 29.4 2.2 1309 6 US-10-449-902-20908 29.4 2.2 1489 6 US-10-449-902-20839 29.4 2.2 1906 6 US-10-449-902-20839 29.4 2.2 1946 6 US-10-449-902-20839 29.4 2.2 2108 6 US-10-449-902-21520 29.4 2.2 2108 6 US-10-449-902-21520 29.4 2.2 2108 7 US-11-121-154-48 29.4 2.2 2367 7 US-11-121-154-48 29.4 2.2 16032 6 US-10-449-902-1155 29.2 23168 6 US-10-449-902-1159 29.3 3168 6 US-10-449-902-11296 28.8 2.2 3457 7 US-11-293-697-1224 28.8 2.2 3457 7 US-11-293-697-1224 28.8 2.2 5862 6 US-10-505-928-25
0; GCACCCAGA GCTCCCGGT GCTCCCGGT GCTAAATG GCCTAAATG GCTTATCCA	Institution. Tichence.	sequence
Gaps 0, AACGCA 174	. תכ	74, Appl 5189, Appl 68, Appl 36, Appl 36, Appl 17204, Ap 17204, Ap 20839, A 20839, A 20152, A 20152, A 20152, A 21152, A 21152, A 21295, A

RESULT 2 US-11-217-529-79920/c ; Sequence 79920, Application US/11217529

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CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION UNMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Pattentin Ver. 2.1
SEQ ID NO 2180
LENGTH: 2879
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FÜÜIMÜRA, TOMOKO
APPLICANT: ASHKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GE
FILE REFERENCE: S-38-285
CURRENT FILLING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PATENTIN VERSION 3.3
SOFTWARE: PATENTIN VERSION 3.3
SOFTWARE: PATENTIN VERSION 3.3
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US-11-293-697-2180/c
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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79920
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APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAMURA, NORIHI
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US20060099612A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                   Match 2.6%;
Local Similarity 50.6%;
                                                                                328
268
                                                                                                                     194 AACTGGGTGAGCTGACACCGCGCGGGGGGGGGGGAGATCGCCTATCTCGGACATTACTGGC
                                                                                                                                                                                         134 CCAAGGCCACCGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCAACCTGGCCGGTAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      671 CCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTC 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 TCCTGCAACAAGCACAGG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 CCGAGTCTGTCTCAAAAATGGGTTTGGTGAGCGTGCCATCAGCGCTGAAGGAGCCGTATT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                GCATGGTGTGGCGGAAGTCGCCCAGCGGGGCGCTGATCATCTCGGCCGTGAGGTCCGCTC
GGGAACGGCGTTGGAGTGCACCGAGCTGGACACCAGTTGCT 227
                                       GTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCT 295
                                                                                                                                                              CCGCGGCCTTGCTATTGAGGAAGGAGGTGTCCCCAAAGGCGTCTCCGGCCCGGCCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATCCAATCCGTAGAGG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKAMURA, NORIHISA
KODAMA, YUKIKO
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Pred. No. 0.061;
0; Mismatches 27;
                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                               Score 34; DB 7; Length 2879; Pred. No. 0.19; 0; Mismatches 80; Indels
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RESULT 4

RESULT 6 US-10-449-902-8987

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FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 11004
LENGTH: 2271
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-10-953-349-11004
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US-10-953-349-27515/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27515, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
FULE REFERENCE: 2750-1579PUS2
CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27515
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                             Query Match 2.5%;
Best Local Similarity 48.4%;
Matches 90; Conservative
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Best Local Similarity
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                                                                                                                                                       1107
                                                                           1047
                                                                                                                                                                                                                                   1167 TAACCTTTAGGTACATCTTGCAGGTTCTACCAACAGGTAAGCTTAACAGCTGACAGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1674 CCTGCGAAAACTAGTTTGCTCTTTGATCTTT 1644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1734 TGAACCGGGACATGTTCGGGTGATATGTACCTGAGAAGGGTTTCTGCAGATCTTGAAGGA 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1212 TGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAATCGTGAATGA 1271
987
                                                                                                              603 TAMACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTCAA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55;
                                    TTCACA 788
                                                                                                                                                                                            GGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGA 722
                                                                           TTTACA 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%;
ilarity 60.4%;
Conservative
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                                                                                                                                                                                                                                                                                                             Score 32.4; DB 6;
Pred. No. 0.46;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                      Length 1393;
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                                                                                                                                                                                                                                                                                                                   Indels
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PRIOR FILING DATE: 2002-05-30
PRIOR PELICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 8987
LENGTH: 1396
                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13868
LENGTH: 2634
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Publication No. US20060123505A1
                                                                                                   Query Match
Best Local Similarity
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                                                                               Matches
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                                                                                                                                                                                               TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK111216
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: OTYZA BATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK106335
DATABASE ENTRY DATE: 2002-08-28
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APPLICANT: Bio-oriented Technology Research Advancement Institute APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A020SYI-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
199 GGTGAGCTGACACCGCGCGGTGGTGAGCTAATCGCCTATCTCGGACATTACTGGCGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGG 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCTCGTTCTCGGTCGCGGTCGCCTTCTCGCCGAAGCGGGAGGAGCTCGTACTCCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTCTCCTGCAA
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                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4%;
                                                                                                   2.4%;
                                                                         Score 31.8; DB Pred. No. 1.1; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
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Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6; Length 1396;
                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40; Indels
                                                                                                                       Length 2634;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institution.
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GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT PILING DATE: 2003-05-29

FRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR FILING DATE: 2002-15-30

PRIOR FILING DATE: 2002-15-11

NUMBER OF SEQ ID NOS: 56791
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US-10-449-902-13863/c
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                                                                                                        GENERAL INFORMATION
                                                                                                                                Sequence 10760, Application US/10449902
Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13863
LENGTH: 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: OTYZB BBLIYB
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK111211
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 2.48;
Similarity 47.78;
                                                                                                                                                                                                                                                                                            ACCAGGAGTGCTG 2750
                                                                                                                                                                                                                                                                                                                                           GCCCGGAGAGGTG 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAAGTTCCGGAGCTCAGACTGCCGCTGCCATGCCTTGCGCTTGAGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                 GGTGAACCCGGAGATGTTGGAGAGCATGGAGGAGGAACGGCCGCCGCCATTGCGGAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCC 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGTGGAACGGGTTACCGAGTTGGAAGCCAGAGGGTGAGTGCGGCTCGTCGAAGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTC
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Mismatches 101;
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US-10-449-902-15013
; Sequence 15013, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-11-293-697-707
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                                                                                                                                                             RESULT 11
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR PRIOR PRIOR DATE: 2002-05-30
PRIOR PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR PRIOR DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 707, Application US/11293697 Publication No. US20060105376A1 GENERAL INFORMATION:
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SEQ ID NO 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.
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ORGANISM: OTYZA BATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108108
DATABASE ENTRY DATE: 2002-08-28
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Local Similarity 53.8%;
                                                                                                                                                                                                                               1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 GATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAAGCCTTCGCCGCCGGGC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 GCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCGCAGTCTGGTCAGGTCGC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 TGŤTGŤTĠĊCĠTTĠŤĊĠĀĊĠĀĠĠĠĀGTĊGCCGĀĀCĀCĠĀĀĠĀĀĠĠĊCCGCTČCGĊĠĠĀĊ 171
                                                                                                                                                                                                                                                                                                                                                                59 CATTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATG 118
                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2791
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                                                                                                                                                                                                                                                                       GTGTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAG 169
                                                                                                                                                                                                                                                                                                                        CCTTCGCAGTGAGTGTTACAGCTCTTAAGGCGGTGTGTCTGGAGTTGTTCATTCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGGTTCGTGGTCTCGCTGGCCTCAGAAGTGAAGCTGCAGATCTTCGCGG 1309
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  2.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 7; Length 2791;
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APPLICANT: SCHWITT, Armin
APPLICANT: SCHWITT, Armin
APPLICANT: LOOK, Maxime P.
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT FILING DATE: 2004-12-11
CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DCT/EP2003/010881
PRIOR APPLICATION NUMBER: DC 10317955.0
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2003-01-07
PRIOR PILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2003-01-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: OTYZA BALÍVA
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK065548
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-15013
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US-10-517-441-65/c
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SEQ ID NO 15013
LENGTH: 3553
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TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-303870
PRIOR APPLICATION NUMBER: JP 2002-303870
PRIOR FILING DATE: 2002-12-11
NUMBER: OF SEQ. ID NOS: 56791
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APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
NUMBER OF SEQ ID NOS: 2147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGTCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGCAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAAGCCTTCGCCGCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGA 416
                                                                                                                                                                                                                                                                                                                                                                                                                               RUJAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIMMRICH, Inko
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Pred. No. 3;
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RESULT 14
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US-10-449-902-965/c
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Sequence 18030, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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Best Local S
Matches 60
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Publication No. US20060123505A1
GENERAL INFORMATION:
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LENGTH: 3050
TYPE: DNA
ORGANISM: Homo Sapiens
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205YI-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOPTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Oryza sativa
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK059042
DATABASE ENTRY DATE: 2001-12-06
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Pred. No. 1.3;
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SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 18030

LENGTH: 772

TYPE: DNA
ORGANISM: OTYZA SATIVA
ORGANISM: OTYZA SATIVA
DATABASE ACCESSION NUMBER: AK068443
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18030
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US-11-289-102-50/c
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LENGTH: 3452
                                                                   Matches
                                                                                                     Query Match
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                                                                                                                                                                                                                                       TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS FILE REPERENCE: 1038 NP CURRENT APPLICATION NUMBER: US/11/289,102 CURRENT FILING DATE: 2005-11-29 PRIOR APPLICATION NUMBER: US 60/631,993 PRIOR PELICATION NUMBER: 004-631,993 PRIOR PELICATION NUMBER: 005-395 PRIOR PELICATION NUMBER: 2004-11-30 NUMBER OF SEQ ID NOS: 395 SOPTMARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lee, Hyerim
APPLICANT: Shaw, Peter M.
APPLICANT: Clark, Edwin
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                               Local Similarity hes 45; Conserv
997 GGCGGCGCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCCAGGT 1056
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ilarity 45.3%;
Conservative
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                                                                                  Pred. No. 5.6;
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Pred. No. 1.9;
0; Mismatches 133;
                                                               Mismatches
                                                                                                     7;
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Search Job ti	뫄	Ş	Db
Search completed: June 14, 2006, 14:23:14 Job time : 39.7719 secs	357 GGGCACTGG 348	1057 GGTGAACTGG 1066	417 GACGTTGCGCTTGAGCCCCGTCTAGACCTCGCTGGCTGAGGGTGATGACATGCCCGGCAGGT 358

Thu Jun 15 11:39:03 2006

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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14.5	14.8	14.8	15.1	19.4	22.6	22.6	26.7	28.3	28.3	28.5	33.9	34.2	36.9	37.3	40.1	40.6	44.4	45.3	Query
546	208	208	320	707	354	706	531	383	383	393	864	868	895	595	529	746	853	616	Query Match Length
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BJ040796	BM412806	BM409016	BE436403	BJ619443	AA545747	CN759004	BU713769	AW036134	AW036132	BE520240	CN757565	CN754382	CN762997	CF326092	BU713770	CA093060	CL662734	BJ074127	ID
BJ040796 BJ040796	o	BM409016 EST583343	BE436403 EST407481	BJ619443 BJ619443	AA545747 HBMSF1B4-	CN759004 ID0AAA24B	BU713769 SJAABUG01	AW036134 EST274510	AW036132 EST274508	BE520240 M11B12STM	CN757565 IDOAAA1DF	CN754382 ID0AAA12D	CN762997 IDOAAASDC	CF326092 JMT105-	BU713770 SJAABUG02	CA093060 SCCCCL200	CL662734 PRI0142b	412	Description

Query Match Best Local Similarity

45.3%;

Score 592; DB 2; Length 616; Pred. No. 4.9e-175;

ALIGNMENTS

ribrary	ORIGIN
/ CLORE 1 ib="NIBB Mochii normalized Xenopus tailbud	
/uDx.ret="caxon:0355" /clone="XLO90j06" /ricauc="XLO90j06"	
/moltpe="mRNA"	
/organism="Xenopus laevis"	acurca
	FEATURES
http://xenopus.nibb.ac.jp.	
The information of this clone is available through the following URL.	
National Institute of Genetics	
Center For Genetic Resource Information	
Contact: Tadasu Shin-i	COMMENT
Expressed genes in X. laevis embryo	TITLE
Kohara, Y.	
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and	AUTHORS
1 (bases 1 to 616)	REFERENCE
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	ORGANISM
Xenopus laevis (African clawed frog)	SOURCE
	KEYWORDS
BU074127.1 GI:17504316	VERSION
laevis cDNA clone XL090j06 5', mRNA sequence.	ACCESS TON
NIBB Mochii normalized Xenopus tailbud library	DEFINITION
BNA	LOCIE
	RESULT 1

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AUTHORS
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Srinivasan, J., Otto, S....
AppaDB: an AcedB database
Pristionchus pacificus
Pristionatus Res. 32 (1)
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PRI0142b_B11 - |
pacificus var. (
         Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                       Pristionchus pacificus
Pristionchus pacificus
Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                     Contact: Sommer RJ
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                                                                                  CA093060
SCCCCL2001D10.b CL2 S
3', mRNA sequence.
CA093060
CA093060.1 GI:349463
BST.
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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Local Similarity
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Class: fosmid ends.
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                             AGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT
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                                                                                                                                                         CCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGA
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AGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
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/mol_type="genomic_DNA"
/strain="California"
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GI:34946367

Saccharum

746 bp mRNA marum officinarum

CDNA

clone SCCCCL2001D10

EST 23-SEP-2003

linear

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centro de Biologia Molecular e Engenharia Genetic Universidade Estadual de Campinas Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137 Fax: 55 19 3788 1089 Exail 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.bcccenter.fcav.unesp.br
Plate: 001 row: D column: 10
Seq primer: M13/Forward primer.
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                  ATCACCGATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTG
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AACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAA
                                                                                               GTGCTGTTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTC 1014
                                                                                                                                                                                        ACAGCGTTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGACATTACCCACTTCA 954
                                                                                                                                                                                                                                CTACAACGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAG
                                                                                                                                                                                                                                                            CTACAACGCACGCCAGAGGTTGCCCCGCAGCCGCCCACCCCCGTTATTAGATTTGATCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="CL2"
/clone lib="CL2"
/note="Organ: Pool of sugarcane calli submitted to low
(4oC) and high (37 C) temperature stress; Vector:
pBlurScript; Site 1: EcoRI; Site 2: XhoI; An
unidirectional cDNA library generated from [Pool of
sugarcane calli submitted to low (4oC) and high (37 C)
temperature stress]. CDNA was prepared from polyA+ mRNA
using ZAP - cDNA Synthesis Kit (Stratagene). The
double-strand cDNAs were fractionated in a sepharose CL-2B
40cm-columns and fragments sizing between 0.8 and 1.5 Kb
were directionally cloned into the vector. Details of
each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Saccharum officinarum"
/mol type="mRNA"
/db_xref="taxon:4547"
/clone="SCCCCL2001D10"
/lab_host="XL1Blue MRF/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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VERSION
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Schistosoma japonicum
Ekkaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Ekkaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 529)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Wang,S.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
Evolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conteat: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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BU713770
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/Clone lib="Mouse and rabbit"
//lab_host="Mouse and rabbit"
//clone lib="Adult worms"
//slone lib="Adult worms"
//clone lib="Adult SjC 7/94"
//note="Wector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from Pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library, First strand synthesis was
primed with an oligo-dT-XhoI-primer and synthesis was
primed with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRi linkers,
digested with EcoRi and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Schistosoma japonicum"
/mol type="mRNA"
/strain="Chinese (Anhui) strain"
/db xref="taxon:6182"
/sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="Whole body"
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ACCESSION
VERSION
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ORGANISM
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CF326092/c
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                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnollophyta; Lillopsida;
clade; Ehrhartoideae; Oryzeae; Oryza.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea
                                                                I (bases 1 to 595)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                 CF326092

JMT1--05-B09.gl AtJMT-overexpressing transgenic rice lambda cDNA library (JMT1) Oryza sativa (japonica cultivar-group) clone JMT1--05-B09, mRNA sequence.

CF326092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTA 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     japonicum sequences."
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Pred. No. 1.3e-153;
0; Mismatches 3;
                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
a; Poales; Poaceae; BEP
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FOCUS

COMMENT

TITLE AUTHORS

REFERENCE

KEYWORDS

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KEYWORDS
SOURCE
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   ORGANISM
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Best Local
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EST.
Acyrthosiphon
Acyrthosiphon
                                             mRNA sequence.
CN762997
CN762997.1 GI
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IDOAAASDC09RM1
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82 31 321 6355
1: bhnahm@ggbio.com, bhna
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/lab_host="E.coli SOLR"
/clone_lib="Rc.WT-overexpressing transgenic rice lambda /clone_lib="AtJWT-overexpressing transgenic rice lambda phage cDNA library (JWT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mrNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT1--05-B09"
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                                              GI:47536920
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pisum
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                 (pea
                                                                                        Acyrthosiphon
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Pred. No. 3.1e-142;
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pisum cDNA clone
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PCR Primers
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UMR B103P, BP 35327, F-35653 Le Rheu Cedex
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
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Unpublished (2004)
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1 (Dases 1 to 895)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
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TACGCCGCCCGGAGAGGTGAAACTGACCCTGGCAGGATGTGAAGAGCGAAATGCGCAGGG 1232
                                              GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA 536
                                                                         GGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAA 1172
                                                                                                                                                                                                                                                                                                                                                        TGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGCAAA 992
                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAGGCGTA
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                                                                                                                                      AGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA
                                                                                                                                                                      AGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCA 1112
                                                                                                                                                                                                                                                                               TCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCCCCGGTCAGCCGGATAACACGCCGCC 1052
                                                                                                                                                                                                                                                                                                                             TGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGCAAA
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/clone lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
/sample name: IDOAAA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: (0)(6/1999);
Harvesting date: 00/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction.; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XI1-Blue"
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/mol_type="mRNA"

/cultivar="developmentstage"
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/clone="IDOAAA5DC09"
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Local Similarity

Conservative

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898 810

839 AACGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCCGTTATTAGATTTGATCAAGACAG

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Query Match
Best Local Sim:
Matches 459;
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1 (bases 1 to 868)

1 Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
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CN754382
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
Contact: D. Tagu
INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aph
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Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 12 row: E column: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics in collaboration with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN754382.1 GI:47519379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: CAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR PRimers
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                                                                                                     /clone_lib="ApMS"
//clone_lib="ApMS"
//note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
//note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
//sample name: IDOAAA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 00/6/1999;
Soil conditions: Soil; Sowing date: 00/6/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction: , experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="developmentstage"
/db_xref="taxon:7029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Acyrthosiphon pisum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IDOAAA12DE01"
                       34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F-35653 Le Rheu
  Score 446.8; DB 8; Pred. No. 4.2e-129; D; Mismatches 2;
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ORIGIN

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RESULT 8
CN757565/c
LOCUS
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ORGANISM
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UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33.2.23.48.51.65

Fax: +33.2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

Risk of contamination by bacterial sequences werk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 864)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                              (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                      PCR PRimers
FORWARD: CAGGAAACAGCTATGACC
Plate: 1 row: F column: 9.
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
CN757565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN757565 864 bp mRNA linear EST 20-MAY-200 IDOAAA1DF09RM1 ApmS Acyrthosiphon pisum cDNA clone IDOAAA1DF09 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN757565.1 GI:47531488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACGCTTCCCCGGTCAGCCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCT 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACT 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGATGCGTGATAAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGA
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                     /clone="IDOAAA1DF09"
/tlssue type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic
/lab host="XL1-Blue"
/clone_lib="ApMS"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1:
                                                                                                                           /organism="Acyrthosiphon pisum"
/mal_type="mRNA"
/cultivar="developmentstage"
/cul_xref="taxon:7029"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pea aphid Acyrthosiphon
      EcoRI; Site_2: XhoI;
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Matches 455;
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                                                                                          GGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAAT 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTGTT
CGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                                                                                                                                                      GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAGAGGTGAAACTGACCCT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCTGGCG 108:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGA-TTGATCAAGACAGCGTT
                                                                                                                                                                      GATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACCCT
                                                                                                                                                                                                                                                                                                               TCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAGCA 1142
                                                                                                                                                                                                                                                                                                                                                                                             GCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGCCCATCCACCGCAAAAAACAGGCGTATGGTGACATTACCCCACTTCAGTGCTGTT
                                                       GGCAGGATGTGAAGAGCGAAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sample name: IDOAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless dults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
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JOURNAL
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ORGANISM
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BE520240/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                    Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
                                                                                                                             1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone M11B12 5', mRNA sequence BE520240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE520240 393 bp mRNA linear EST 19-MAR-2001 M11B12STM Arabidopsis developing seed Arabidopsis thaliana cDNA
Michigan State University
224 Biochemistry, Michigan
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  State University,
     East
  Lansing,
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REFERENCE
AUTHORS
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AW036132
LOCUS
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VERSION
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ORGANISM
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Best Local Similarity
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Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
Lycopersicon.

1 (bases 1 to 383)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,P., Upton,J., Ronning,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C.,
                                                                                                                                                                                                                               AW036132

AW036132

EST274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone cLEEIEZ3 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036132
                                                                                                                                                                                             EST.
                                                                                                                                                                                                              AW036132.1 GI:5894811
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Fax: 517 353 9334
Email: benning@meu.edu
Email: benning@meu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany
Zoology Biddy. 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTCATTAACCGGTGCGGTAAGCCTCGCATCA 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: p
Site_1: EcoRI; Site_2: XhoII"
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/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="M11B12"
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Pred. No. 5.4e-106;
0; Mismatches 13;
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VERSION
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LOCUS DEFINITION RESULT 11 AW036134/c

AW036134
383 bp mRNA linear EST 18-MAY-2001
EST274510 tomato seed, TAMU Lycopersicon esculentum cDNA clone
cLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase
precursor, putative, mRNA sequence.
AW036134

SOURCE ORGANISM

EST AW036134.1

GI:5894813

Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

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Best Local Similarity
Matches 375; Conserv
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JOURNAL
361
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Contact: CUGI
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.genome.clemson.edu/orders/index.html
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ATCAATGCTGACGGAGATATTTC
                   ATCAATGCTGACGGAGATATTTC
                                                           ACCATCGGAACTCAAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGC
                                                                                ACCATCGGAACTCAAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGC
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/lab_host="XL1-Blue MRF'"
/clone_libertcomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site
Xho1; cLEE - Tomato Seed EST Library. Directionally cl
CDNAs inserted into pBlueScript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEE1E23"
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Pred. No. 5.5e-105;
0; Mismatches 8;
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BU713769.1
EST.
                                                                    BU713769
                                                                                                      6-PHYTASE ], mRNA sequence.
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/clone_lib="tomato_seed, TAMU"
/clone_ib="tomato_seed, TAMU"
/note="Vector: pBlueScript_SK(-); Site_1: EcoR1; Site_2:
Xho1; cLEE - Tomato_Seed_EST_Library. Directionally cloned_cDNAs_inserted_into_pBlueScript_SK(-) at 5' end_with_EcoR1 and 3' end_with_Xho1_site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4081"
/clone="cLEB1E23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Lycopersicon
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                                  GI:28321125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 370.2; DB 7;
Pred. No. 5.5e-105;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8,
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CTCCTGCAACAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGGATCACCGATTCACAC 789

CTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACAC 120

GCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT 729

GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG 60

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REFERENCE
AUTHORS
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PUBMED
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                                  Local Similarity
   425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 531)

Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.

Evolutionary and biomedical implications of a Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schistosoma japonicum
Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complementary DNA resource
26.7%;
llarity 88.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genet. 35 (2), 139-147 (2003)
                                                                                                                                                                                                                                       /db xref="txanus" | Brain | Ab xref="txanus" | Ab x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hanzg@chgc.sh.cn
                                                                                                                                                                                                                    Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Schistosoma japonicum"
/mol_type="mRNA"
/strain="Chinese (Anhui) strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                     japonicum sequences.
   0
                                      Score 348.6;
Pred. No. 4.1
   Mismatches
                                  4.1e-98;
                                                                         DB 3;
   54;
   Indels
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4:
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RESULT 13
CN759004/c
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                               Bource
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                                                                                                                                                                                                                                PCR PRIMETS
FORWARD: CAGGAAACAGCTATGACC
Plate: 24 row: C column: 4.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Sternorrhyncha; Aphidiformes;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 706)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D.; Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDOAAA24BC04RM1 ApMS Acyrthosiphon pisum cDNA clone IDOAAA24BC04
5', mRNA sequence.
CN759004
CN759004.1 GI:47532927
                                                                                                                                                                                                                                                                                                        Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                               UMR BiO3P, BP 35327, PTel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2004)
Contact: D. Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                 INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CN759004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGT: 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGG-TGTTTGAACGCT-GGCGTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGTTGCCCGCAGCCGCACCCCGGTATTAGATTTGATCAAGACAGCGTTGACGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTANGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGAC-TTACAGCAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGCAGCCCGATAACACGCCCGCAGGAGCGGAACTGGATGTTTGAACGCTGGGCGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTTTATCATTATGATTTGCATGTGGAGAGACAATTCCCTCTTGAGTGACGAAAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482
/clone_lib="ApMS"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
/mote="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
// Sample name: IDOAAA ; Plant growth place: Department of
// Ecology & Evolutionary Biology, Princeton University;
                                                                                                                                    /organism="Acyrthosiphon pisum"
|mol type="mRNA"
|cultivar="developmentstage"
|db xref="taxon:7029"
|clone="IDOAAA24BC04"
                                                                                   /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XII-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                               F-35653 Le Rheu Cedex France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     database for the pea aphid Acyrthosiphon
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AUTHORS
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VERSION
KEYWORDS
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AA545747/c
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JOURNAL
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Matches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                         Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1182
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Local Similarity
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                                                                                                                                                                                                                                                                                         Email: libin@helix.nih.gov
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.

1 (bases 1 to 354)

1 (bases 1 to 354)

Jia,L., Robey,P., Young,M., Schuler,G., Powell,J., Yang,L.,
Jia,L., Robey,P., Young,M., Bowles,L., Geisel,S., Kucaba,T.
Lennon,G., Hillier,L., Allen,M., Bowles,L., Geisel,S., Kucaba,T.
Marra,M., Martin,J., Steptoe,M., Tan,F., Theising,B., Bowers,Y.,
Wylie,T., Waterston,R., Wilson,R. and Francomano,C.
WashU-MGB/NHGRI EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA545747

ABMSF1B4-REV Human Bone Marrow Stromal Fibroblast Homo sapiens clone HBMSF1B4 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA545747
AA545747.1 GI:2307026
                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-402-4877
Pax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                          National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Libin Jia
Medical Genetics Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTGGCAGGTTTTACGCAAATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCACTGGAGCTCAACTGGACGCTTCCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTCTTCCAGACTTTACAGCAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCC 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTGGTGTTTGAACGCTGGCGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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/sex="Male and Remale"
/tissue_type="bone marrow"
/cell_type="stromal fibroblast"
/dev_stage="mixed"
/lab_host="XL1-Blue"
                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                       'clone="HBMSF1B4"
                                                                                                                                                                                                                                                                      . 354
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99.3%;
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Pred. No. 2.1e-81;
D; Mismatches 2;
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>mo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kucaba, T.,
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TITLE
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COMMENT
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AUTHORS
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ORGANISM
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BJ619443
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499 CTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCATTATCAAACGGCGTTTCGC 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 CAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707 bp mRNA linear EST 01-OCT BJ619443 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL189d24 5', mRNA sequence.
                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 707)

1 (bases 1 to 707)

1 (kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Yokayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T.
                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                        Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                     http://xenopus.nibb.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                               Kohara, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BJ619443.1 GI:37258203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTCAAGGTGAGCGCCGACAAT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTCAAGGTGAGCGCCGACTGT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAACAG 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACTGGAACGGGTG-TTAATTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGATCACCGATTCACACCACTGGAAC
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/note="Vector: pBluescript; Site_1: EcoRI; Site_2: KhoI"
                               /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL189d24"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early
                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                          available through the following
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 241
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                                                                                                                                                                                                                                750 AATGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAACACCTTGCTAAG
                                                                                                                                                                                                                                                                       255;
                                                                                                                                                              61
                                                                      GTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGC
                                                                                                                                CACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAGGC 929
                                                                                                                                                                                                                ANTGCCGGAGCCGGGGTGGGGAAGGATCACCGATTCACACCAGTGGAACACCTTGCTAAG
 AAATCTCGGCGGCGCA
                     AAATCTCGGCGGCGCA 1005
                                                     GTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCCGGACACGATACTAATCTGGC
                                                                                                         CACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAGGC 180
                                                                                                                                                              TITGCATAACGCGCAATTITATTTGCTACAACGCACGCCAGAGGTTGCCCGCAGCCGCGC 120
                                                                                                                                                                                       TTTGCATAACGCGCAATTTGATTTGCTACAACGCACGCCAGAGGTTGCCCCGCAGCCGCGC 869
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                 19.4%;
  256
                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                   Score 254.4; DB 2
Pred. No. 2.6e-68;
                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                 Length 707;
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Search completed: June 14, 2006, 14:21:52 Job time: 6872.62 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                        1308
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seq length: 2000000000
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1: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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15: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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10064.996 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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        10 US-10-933-115-9
14 US-11-056-354-1
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11 US-10-933-115-5
3 US-09-866-379-1
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Sequence 1, Appli
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Sequence 5, Appli
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Sequence 7, Appli
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US-10-156-660-1
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ALIGNMENTS

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Sequence 1, Application US/1015660
Publication No. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Short, Keith
APPLICANT: Gary, Kevin A.
APPLICANT: Gary, Kevin A.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US 09/586,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 1
SEX INFORMATION: modified phytase enzyme
PEATURE:
OTHER INFORMATION: modified phytase enzyme
PEATURE:
OTHER SEQ ID NO (1)...(1308)
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             TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
                                              TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
                                                                                            CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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APPLICANT: Kretz, Keith A.

APPLICANT: Kretz, Keith A.

APPLICANT: Gray, Kevin A.

APPLICANT: Gray, Kevin A.

APPLICANT: Gray, Kevin A.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: O' Donoghue, Eileen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: RECOMBINANT PHYTASES AND MET.

TITLE OF INVENTION: US 09/10/601,319

CURRENT APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 1000-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR FILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/29,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1308
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US-10-601-319-9
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                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: modified phytase en
PEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1296)
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                                                                                                                                                   Matches 1308;
                                                                                                                                                                          Local Similarity
                                                                              ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCCGCAATCTGCA
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100.0%; Pred. No. 0;
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                                                                      CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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RESULT 3
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; Sequence 9, Application US/10933115
; Publication No. US20050281792A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Gray, Keyin A.
; APPLICANT: Gray, Keyin A.
; APPLICANT: Barton, Nelson Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 564462001822

FILE REFERENCE: 564462001822

CURRENT FILING DATE: 2004-09-01

FRIOR APPLICATION NUMBER: US/09/866,379

FRIOR APPLICATION NUMBER: US/09/866,379

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FRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

FRIOR APPLICATION NUMBER: US 09/21,931

FRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOSTWARRE: FRASESEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1308
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US-10-933-115-9
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Best Local Similarity
Matches 1308; Conserv
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APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: modified phytase enzyme FEATURE: NAME/KEY: CDS LOCATION: (1)...(1296)
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                           ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGGTGGTGAGCTAATCGCCTATCTC
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Garrett, James B.
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llarity 100.0%; Pred. No. 0;
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                                                                                                                    CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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Sequence 1, Application US/11056354

Publication No. US20050246780A1

GENERAL INFORMATION:
APPLICANT: KRETZ, Keith
APPLICANT: GARRETY, Jay M.
APPLICANT: GARRETY, James B.
APPLICANT: GARRETY, James B.
APPLICANT: GARRETY, James B.
APPLICANT: GARRETY, James B.
APPLICANT: WATHUR, Exic J.
TITLE OF INVENTION: POR MAKING AND USING THEM AND METHODS
TITLE OF INVENTION: POR MAKING AND USING THEM
FILE REFERENCE: 564462001803/01370-9C1
CURRENT PILING DATE: 2005-02-1
CURRENT PILING DATE: 2005-02-1
PRIOR APPLICATION NUMBER: US 10/156,660
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
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US-11-056-354-1
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Best Local Similarity
Matches 1296; Conserv
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  GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                               GCCTTCGCCGGCCGGGCTGGCACTGTGCAATAACCGTACATACCCAGGCAGATACG
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RESULT 5
US-10-601-319-6
; Sequence 6, Ap
Sequence 6, Application US/10601319
Publication No. US20040091968A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Stort, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Yevin A.
APPLICANT: Garyett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Mathur, Eric J.
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SENOTH: 1901
LENOTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
FEATURE:
NAME/KEY: misc_feature
OCATION: 403
OTHER INFORMATION: n = A,T,C or
US-10-601-319-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING TITLE OF INVENTION: AND USING THEM FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT PILLING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR PILLING DATE: 2001-05-24
PRIOR PILLING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILLING DATE: 1909-05-25
PRIOR PILLING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
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Best Local Similarity
Matches 1280; Conserv
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                                                                            AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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                   CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
                                                                                                                                         TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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pred. No. 0;
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Indels Length

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240 367

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480 607 420 547 360

1901; 0;

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Sequence 5. Application US/10601319

Publication No. US20040091968A1

GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Bileen
APPLICANT: Mathur, Eric J.
APPLICANT: OF INVENTION: AND USING THEM
FILLE OF INVENTION: AND USING THEM
FILLE REFERENCE: 09010-029011

CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/860,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931
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; PRIOR APPLICATION NUMBER: US 09/259,214
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/910,798
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1901
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 403
; OTHER INFORMATION: n = A,T,C or G
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APPLICANT: Kretz, Keith A.

APPLICANT: Kretz, Keith A.

APPLICANT: Gray, Kevin A.

APPLICANT: Gray, Kevin A.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: O' Donoghue, Eileen

APPLICANT: O' Donoghue, Eileen

APPLICANT: O' TONOGHUE, EILEEN

APPLICANT: O' DONOGHUE, EILEEN

APPLICANT: O' TONOGHUE, EILEEN

ITTLE OF INVENTION: FECOMBINANT BACTERIAL PHYTASES AND USES

ITTLE OF INVENTION: FILEROF

FILE REFERENCE: 564462001822

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/290,214

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 08/910,798

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                                                       TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACACTTTACCCACTTCAGTGCTG
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                                   TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
                                                                                                          CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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QY 121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA	Qy 61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT	Qy 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTGATTCCGTTAACCCCGCAATCTGCA	Query Match 96.7%; Score 1265; DB 3; Length 1323; Best Local Similarity 98.0%; Pred. No. 0; Matches 1280; Conservative 0; Mismatches 26; Indels 0;	NAME/KEY: misc_feature; LOCATION: (1)(1323); OTHER INFORMATION: n is any nucleotide US-09-777-566A-1	; ORGANISM: Escherichia coli ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)(1320)	SOFTWARE: Patentin version 3.0 SEQ ID NO 1 LENGTH: 1323 TYPE: DNA	PRIOR FILING DATE: 1999-03-01 PRIOR APPLICATION NUMBER: US 08/910,798 PRIOR FILING DATE: 1997-08-13	PRIOR FILING DATE: 1999-05-25 PRIOR APPLICATION NUMBER: US 09/291,931 PRIOR FILING DATE: 1999-04-13 PRIOR FILING DATE: 1999-04-13	THOUGH AND CODE	APPLICANT: DIVERSA CORPORATION APPLICANT: SHORT, Jay APPLICANT: KRETZ, Keith TITLE OF INVENTION. BECOME TRANSPORT OF PROPERTY.	US-09-777-566A-1 ; Sequence 1, Application US/09777566A ; Patent No. US2001005578BA1 . CRUEDAL TURCOMATION.	1448	Db 1388 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300	1201	Qy 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC	QY 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG	Oy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG [QY 961 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
Qy 12 Db 12	120 Qy 120 Db	60 Db			9 da	Qy 8 Db 8	Qy 7 Db 7	Qy 7	Qy 6	Dp 6	Qy 5	Qy 4	ACGCAA 1447 Qy 4	1260	CTGACC 1200 Db 3	TTACAG 1140 Db 2 TTACAG 1327 Qy 3	CGCTGG 1080 Db 1 CGCTGG 1267 Qy 2	1020
01 CTGGCAGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260 	1 CAGATIGGETGATAAAAGGCCGCCIGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGAACCTGACCGCCGGAGAGGTGAAAACTGACCGCCGGAGAGGTGAAAACTGACCGCCCGGAGAGGAGGTGAAACTGACCGCCCGGAGAGGAGGTGAAACTGACCGCCCGGAGAGGAGGTGAAACTGACCGCCCGGAGAGGAGGTGAAACTGACCGCCCGGAGAGGAGGAGGAGAACTGACCGCCGCCCGGAGAGAGGAGGAGAACTGACCGCCCGGAGAGAGGAGAGAGA	BI CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG BI CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG	ACGCTTCCCGGTCAGCCGGATAACAGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 	61 TTTATIGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG	01 TTGACGCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 960 	41 CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG 900	81 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA 840	21 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC 780	61 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	01 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 660 	41 TATCANACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600	81 AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540	21 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG 480		01 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGGCTACATACCCGTAAAACAGGCGAA 360 61 GCCTTCGCCGGCGGGGTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 420	41 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGACGGA	81 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240 41 GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGATTGCCTGCC	21 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180 81 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGGGTGGTGGTGATCGCCTAATCTC 240

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Sequence 1, Application US/09866379
Patent No. US20020136754A1

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GARTON, Nelson
APPLICANT: GARTON, Nelson
APPLICANT: O'DONGGHUE, Elleen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PH)
FILE REFERENCE: DIVER1370: US/09/866,379
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.1
ENGITH: 1323
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US-09-866-379-1
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LOCATION: (1)..(1323)
OTHER INFORMATION: n is any m
NAME/KEY: CDS
LOCATION: (1)..(1323)
OTHER INFORMATION:
US-09-866-379-1
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Best Local Similarity 98.0%;
Matches 1280; Conservative
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ORGANISM: Escherichia coli
FEATURE:
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; Publication No. US20030049815A1
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CURRENT APPLICATION NUMBER: US/10/034,985

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: US/09/580,515

PRIOR APPLICATION NUMBER: US/09/580,515

PRIOR PILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR PILING DATE: 1997-08-13

PRIOR APPLICATION NUMBER: 09/259,214

PRIOR APPLICATION NUMBER: 09/259,214

PRIOR APPLICATION NUMBER: 09/259,214

PRIOR APPLICATION DATE: 1999-03-01
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ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
COTHER INFORMATION: n = A,T,C or
US-10-034-985-1
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Best Local 9
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               ATCGTGAATGAAGCACGCATACCGGGGTGCAGTTTGAGATCTCATC 1306
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                                                                                       CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                                                    CAGATGCGTGATAAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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US-10-430-36-1
US-10-430-356-1
Sequence 1, Application US/10430356
Publication No. US20030232041A1
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION NOVEL PHYTASE
FILE REFERENCE: 0901/02903
CURRENT APPLICATION NUMBER: US/10/430,356
CURRENT FILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 09/299,214
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli

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Best Local Similarity
Matches 1280; Conserv
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NAME/KEY: misc_feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C
-10-430-356-1
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                                                                                          GATTCACACCAGTGGAACACCCTTGCTAAGTTTGCATAACGCGCCAATTTGATTTTGCTACAA
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                                      CGCACGCCAGAGGTTGCCCCGCAGCCGCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG
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TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
                         CGCACGCCAGAGGTTGCCCCGCAGCCGCCACCCCGTTATTGGATTTGATCATGGCAGCG
                                                                            GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
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(1)...(1320)
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Pred. No. 0;
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APPLICANTAL MATHUT, EFIG J.

APPLICANTAL MATHUT, EFIG J.

FIITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING TITLE OF INVENTION: AND USING THEM FILE REFERENCE: 09010-029011

CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT FILING DATE: 2003-06-20

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 1099-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1999-03-01
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US-10-601-319-1
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Publication No. US20040091968A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
                                                                                                                          LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia c
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
PEATURE:
NAME/KEY: misc_feature
LOCATION: 216
OTHER INFORMATION: n = 1
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APPLICANT:
APPLICANT:
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Garrett, James B.
O' Donoghue, Eileen
Mathur, Eric J.
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Query Match

96.7%;

Score 1265;

DB 8;

Length 1323;

98.0%;

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Best Local Similarity 98.( Matches 1280; Conservative
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                   ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
                                                                         TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020
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RESULT 13

US-10-933-115-1

Sequence 1, Application US/10933115

Publication No. US20050281792A1

Publication No. US20050281792A1

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith A.

APPLICANT: Garyett, Jay M.

APPLICANT: Garyett, Jayes B.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES TITLE OF INVENTION: THEREOF

FILE REFERENCE: 564462001822

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/290,214

PRIOR APPLICATION NUMBER: US 09/290,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1999-08-13

NUMBER OF SEO ID NOS: 10
                                                                                                                                                                                                                                                                            SEQ ID NO 1

LENGTH: 1323

TYPE: DNA
ORGANISM: Escherichia ci
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
FEATURE:
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                                                                                                                                Query Match
Best Local Similarity
Matches 1280; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 216
OTHER INFORMATION: n =
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                                                                                                                              ; Score 1265; DI
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Sequence 7167, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Wang, Liangsu

APPLICANT: Malone, Cheryl

APPLICANT: Trawick, John

APPLICANT: Trawick, John

APPLICANT: Yamamoto, Robert

APPLICANT: Yamamoto, Robert

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Gen

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7167
LENGTH: 1299
TYPE: DNA
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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
ITITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REPERENCE: DIVER1370-7
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/866,379
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR TILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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; LCCATION: (1)...(1901)
OTHER INFORMATION: n is any nucleotide
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US-09-866-379-6
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Best Local Similarity
Matches 1277; Conserv
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Search completed: June 14, 2006, 12:41:32 Job time: 1599.84 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query No. Score Match Length DB ID Description 1 1308 100.0 1308 10 ADC87742 Adc87742 DNA encod 2 1308 100.0 1308 15 AEE75420 Aec75420 E. coli B 4 1296 99.1 1296 14 AED50817 Aec75422 E. coli B 5 1294.2 98.9 1901 12 ADC50296 Adc50295 Escherich 7 1267 96.9 1901 12 ADC50295 Adc50295 Escherich 8 1267 96.9 1901 12 ADC50295 Adc50295 Escherich 9 1267 96.9 1901 12 ADC50295 Adc50295 Escherich 10 1265 96.7 1323 5 AAC68885 11 1265 96.7 1323 6 AAD36473 Aec75416 E. coli p 1265 96.7 1323 6 AAD36473 Aed5473 Becherich 11 1265 96.7 1323 8 ADA19445 12 1265 96.7 1323 12 ADC50201 Adc50291 Escherich 12 1265 96.7 1323 12 ADC50201 Adc50201 Escherich 13 1265 96.7 1323 12 ADC50301 Adc50201 Escherich 14 1265 96.7 1323 12 ADC50301 Adc50301 Escherich 15 1265 96.7 1323 12 ADC50301 Adc50301 Escherich 16 1265 96.7 1323 12 ADC50301 Adc50301 Escherich 17 1264 96.6 1299 8 ACA19297 Prokaryot

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O'donoghue E;								soybean meal; osphate;						Acc57673 Escherich	ACC57672 ESCNE Aad06832 E. co	Aaa28216 E. co	Aad06831 E. co	Adil6138 Shig	Aac68299 SV40/	Ada19452 E. co	Ad102197 DNA	Aac68300 Lama2 Aac68294 Lama2	Aac68295 R15/A	Aac68296 R15/APPA	Aed50824 Esch	Adl16139 Shig	Aee75418 E. c	Ado50297 Esch Aed50819 Esch	Adc87744 DNA	Aad25463 Escherich	6137
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WPI; 2003-787039/74.

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The invention discloses a new isolated or recombinant nucleic acid which CC encodes a polypeptide having a phytase activity. Also claimed is a nucleic acid probe, an amplification primer sequence pair, an expression CC cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic cacid, a transgenic non-human animal or plant, or its seed, comprising the cacid, an antisense oligonucleotide, inhibiting the translation of CC aphytase message in a cell, a heterodimer comprising the polypeptide and comprising an antibody that specifically binds to the cC acid, a hybridoma comprising an antibody that specifically binds to the polypeptide, a food supplement for an animal, an edible enzyme delivery comprising a medible engine pellet comprising a granule edible enzyme delivery colypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, which gain anti-phytase antibody, producing a recombinant polypeptide, determining whether a compound binds to the polypeptide, identifying a modulator, whole cell engineering of new or modified composition, and processing of the phytase polypeptide, increasing the resistance or thermostability of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a cc digestive system and processing of corn and sorghum kernels. The phytase activity comprises catalysis of phytate (myo-inositol-hexaphosphate) to is useful in improving the feeding value of phytate rich ingredients or as an aid in phytate digestion. The sequence presented is the DNA cc encoding the modified Escherichia coli phytase.
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Best Local Similarity 100.

Matches 1308; Conservative
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improving the feeding value of phytate rich ingredients or as an aid
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RESULT 2 AD05029 ID AD05 XX AD05 XX AD05 XX AD05 XX Esch XX Esch XX Esch XX AppA XX AppA XX AppA XX AppA XX Sech XX Sphyth XX Sech XX Synt XX

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ADO50299 standard; DNA; 1308 ₽P.

29-JUL-2004 (first entry)

Escherichia coli K12 appA phytase mutant 819PH59 DNA

AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; gene; mutant; ds.

Escherichia coli; K12

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Location/Qualifiers

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Query Match Best Local Sim Matches 1308;

Similarity

100.0%;

0

0;

Indels

0

Gaps

Score 1308; Pred. No. 0; 0; Mismatches

BB

Length

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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to condified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to cm prove the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present
                                                                                                                                                                                                                                                                                                                                     Short JM,
Mather EJ;
 Sequence 1308 BP;
                                                                                                                                                                                                                                                             Producing phytase, involves encoding polypeptide having
                                                                                                                                                                                                                            Claim 3; SEQ ID
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(GRAY/)
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13-APR-1999;
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) BARTON N R.
) GARRETT J B.
) O'DONOGHUE B.
) MATHER E J.
                       is Escherichia coli K12 appA phytase mutant DNA.
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           CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                  ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTTGAACGCTGG
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CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC

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The present sequence is that of a polynucleotide encoding a novel modified phytase derived from the Escherichia coli appA protein, with improved thermal tolerance and protease stability compared to the wild-type. The present invention relates to a novel formulation, comprising

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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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                                                                                                                                        Formulation useful as dietary supplement for treating, preventing reversing osteoporosis and bone loss, and preventing muscle cramps comprises one or more polypeptides having phytase activity.
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BARTON N R.
GARRETT J B.
ODONOGHUE E.
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99US-00259214.

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CC least one polypeptide having phytase activity, where the polypeptide is a CC modified sequence (AEE75421) derived from the Escherichia coli K-12 appA CC phytase (AEE75419). The modification of the enzyme, comprising a series CC of mutations, improves the thermal tolerance and protease stability of CC the protein. The specification also claims a pharmaceutical composition; CC a kit; an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising CC the novel phytase, and a method of reducing pollution and increasing cC utrient availability in an environment or environmental sample by CC degrading environmental phytic acid. The novel enzyme is a dietary CC supplement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful CC and increasing nutrient availability in an environment or environmental complete by degrading environmental phytic acid, where the environment or CC environmental sample comprises a soil or a body of water. The immobilized CC converse in useful in foodstuffs for improving the feeding value of converse in interestion converse in interestic converse in interestic converse in interestic converse in interestic converse interestic converse converse in interestic converse converse converse converse converse c
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tive 0; Mismatches
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13-AUG-1997; 11-FEB-2005;

97US-00910798

2005US-00056354

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                                                                                                                                                                                                                      animal; gene therapy; feedstuff; food; thermostable; sequence; 3-phytase; recombinant DNA; appA gene.
                                                                                                                                                                                                                                                                                 (first entry)
                                                                                    /*tag= a
/EC number= "3.1.3.8"
/partial
/product= "Bscherichia c
/note= "No stop codon"
                                                                                                                                                              ocation/Qualifiers
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                                                                                                  coli phytase
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Best Local Simi
Matches 1296;
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
24-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also useful in gene therapy and in production of transgenic animals. The present sequence is the SEQ ID NO: 1 which is given in the sequence listing. This sequence differs from the SEQ ID NO: 1 shown on page 19 in disclosure of the specification (see AED50824).
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Mathur EJ;
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(KRET/)
(GRAY/)
(BART/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) ODONOGHUE E.
) MATHUR E J.
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                            GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
                                                                                                                      ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA
                GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
                                                                   CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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                                                                                                       GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG
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 GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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99US-00291931.

99US-00318528.

2000US-00580515.

2001US-00866379.

2002US-00156660.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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100.0%; Pred. No. 0;
tive 0; Mismatches
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gene; mutant; thermostable; phytase; protein stabilization;
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                                                    (first
                       appA phytase 819PH59
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                                                   entry)
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                        DNA sequence SEQ
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1080

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osteopathic; food; appA.
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replace(691,C)
/*tag= 0
                                          /note= "Wild type !
replace(864,A)
/*tag= t
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replace(477,A)
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/note= "Wild type
replace(730,G)
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replace(690,G)
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replace(729,G)
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replace(728,C)
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replace(470,G)
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                              /note= "Wild type
replace(1016,T)
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/*tag= s
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replace(437,C)
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/note= "Wild type
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                                                                                                                                                                                                                                                                                                                                       /note= "Wild type base C replaced
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/note= "Wild type
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                 "Wild type base T replaced by
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120 307

247

TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT

ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTTCTGATTCCGTTAACCCCGCAATCTGCA

ATGARAGCGATCTTRATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA

188

Matches

1296;

Conservative

0

4; 15;

Indels

Gaps

Score 1294.2; Pred. No. 0; 0; Mismatches

Query Match Best Local Similarity

98.9%;

Sequence

1901

BP;

470 A; 497 C; 500 G;

433 Ţ, DB

0 U;

1 Other; Length

1901; 0

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The present sequence is that of a polynucleotide encoding a novel compodified phytase derived from the Escherichia coli appA protein, with compodition proved thermal tolerance and protease stability compared to the wild-cype. The present invention relates to a novel formulation, comprising at compodified sequence (AEE75419) deserved from the Escherichia coli K-12 appA compodified sequence (AEE75419). The modification of the enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition; a kit, an immobilized phytase; a ferrilizer or soil additive; a liquid colluture or cell culture media; and a plant food additive, all comprising nutrient availability in an environment or environmental sample by degrading environmental phytic acid. The novel enzyme is a dietary complement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful cample by degrading environmental phytic acid. The novel enzyme is a dietary complement useful for treating muscle cramps. The liquid supplement is useful comprises a soil or a body of water. The immobilized phytase is useful in foodstuffs for improving the feeding value of compilers useful comprises a soil or a body of water. The immobilized specification but was created from the wild-type sequence (AEE75418) and the information given in claim 1.
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13-APR-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Formulation useful as dietary supplement for treating, preventing reversing osteoporosis and bone loss, and preventing muscle cramp, comprises one or more polypeptides having phytase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page; 82pp; English.
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(KRET/)
(GRAY/)
(BART/)
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24-MAY-2001;
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE B.
BAUM W.
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99US-00291931.
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                   CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGAGGTGAAACTGACC
                                                                                              CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG
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CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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(ODON/)
(MATH/)
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(KRET/)
(GRAY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                ) GARRETT J B
) O'DONOGHUE 1
) MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SHORT J M.
KRETZ K.
GRAY K A.
BARTON N R.
GARRETT J B.
O'DONOGHUE E.
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; 99US-00259214.
; 99US-00291931.
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; 2001US-00866379.
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al feed; fish feed; dough; baking; gene; mutant; ds.
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Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid 2004-374952/35 Ş

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SEQ ID NO 6; 74pp; English

The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially

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CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260

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Query Match
Best Local Similarity
Matches 1280; Conserv
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AppA phytase;
phytate; anima
                                                        Escherichia coli K12 appA phytase mutant DNA
                                                                                                    29-JUL-2004
tase; bacteria; thermal tolerance; prote animal feed; fish feed; dough; baking;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                            ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT
                                                                                                                                                                                                                                                                                   ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT
                                                                                                                                                                                                                                                                                                                                                                                            CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
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                                                                                                (first entry)
                                                                                                                                                                                 DNA; 1901
                                                                                                                                                                                 ВP
            protease stability;
                                                          #1.
gene;
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  mutant;
                    foodstuff;
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AC ADDS0295;

XX 29-JUL-2004 (first entry)

XX 28 Escherichia coli Kl2 appA phytase mutant DNA #1.

XX AppA phytase; bacteria; thermal tolerance; protease s W phytate; animal feed; fish feed; dough; baking; gene;

XX Scherichia coli; Kl2.

XX Synthetic.

XX Location/Qualifiers

FT mutation replace(389,T)

FT mutation replace(390,G)

FT mutation replace(390,G)

FT mutation replace(390,G)

Ytag= a

XX US2004091968-A1.

XX US2004091968-A1.

XX XX IS-ANAY-2004.

XX IS-ANAY-2004.

XX IS-ANAY-2004.

XX IS-ANAY-2004.

XX IS-ANAY-2001; 2003US-00601319.

XX IS-ANAY-2000; 2003US-00601319.

XX IS-ANAY-2001; 2001US-0086379.

XX IS-ANAY-2001; 2001US-00866379.

XX ISHOR/) SHORT J M.

PA (KRET/) KRETZ K.

PA (GAAR/) GARAY T J B.

PA (OLOM) O'DOMOGHUE E.

PA (MATH/) MATHER E J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease comprove the feeding value of phytate rich ingredients, and in diet of CC improve the feeding value of phytate rich ingredients, and in diet of CC incorporate animals including mammals, fowls and fishes, commercially conficient avian species such as pigs, yoats, laboratory rodents, commercially commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present composition, higher yields and loading efficiency. The phytase CC sequence is Escherichia coli KI2 appA phytase mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Short JM,
Mather EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1901 BP;
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               TATCAAACGGCGTTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                                                                                                         GCCTTCGCCGCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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                                                                                                                                           TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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 CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                           AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                              AACGTGACTGACGCGATCCTCGAGAGGGCCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                                     TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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13-AUG-1997;
01-MAR-1999;
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                                           01-SEP-2004; 2004US-00933115
                                                                                                                                   Escherichia
                                                                                                                                                                 fertilizer;
                                                                                                                                                                             ds; thermostable; phytase; protein stabilization; pharmaceutical;
                                                                                                                                                                                                                                          23-FEB-2006
                                                                                                                                                                                                           coli phytase related DNA sequence
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                                                                                                                                   coli.
                                                                                                                                                             cramp;
                                                                                                                                                                                                                                          (first entry)
97US-00910798
99US-00259214
                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                 cell culture; osteoporosis; osteopathic; food
                                                                                                                                                                                                                                                                                                      1901
                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                            SEQ ID
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                                                                                                                                                                                                                                                                                                                                       CC formulation, comprising at least one polypeptide having phytase activity, CC where the polypeptide is a modified sequence (AEB75412) derived from the Escherichia coli K-12 apph phytase (AEB75412). The modification of the CC enzyme, comprising a series of mutations, improves the thermal tolerance CC and protease stability of the protein. The specification also claims a CC pharmaceutical composition; a kit; an immobilized phytase; a fertilizer CC or soil additive; a liquid supplement for preventing muscle cramps; a CC hydrating agent; a tissue culture or cell culture media; and a plant food CC additive, all comprising he novel phytase, and a method of reducing pollution and increasing nutrient availability in an environment or CC environmental sample by degrading environmental phytic acid. The novel CC enzyme is a dietary supplement useful for treating, preventing or compared supplement is useful for preventing muscle cramps. The CC injuid supplement is useful for preventing muscle cramps. The method is useful for reducing pollution and increasing nutrient availability in an convironment or environmental sample by degrading environmental phytic acid, where the environmental sample by degrading environmental phytic acid, where the environmental sample preventing muscle cramps. The method is cody of water. The immobilized phytase is useful in foodstutifs for improving the feeding value of phytate rich ingredients. NOTE: The CC present sequence is shown in the sequence listing but not discussed celsewhere in the specification.
                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 1279;
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25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a DNA sequence related to the production of the novel thermostable / protease resistant Escherichia coli phytase described in the specification. The present invention relates to a novel
                                                                                                                                                                                                                                                                                                      Sequence 1901 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 5; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Formulation useful as dietary supplement for treating, preventing creversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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GRAY K A.
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BARTON N R.
GARRETT J B.
ODONOGHUE E.
DAUM W.
ROBERTSON D II
ZORNER P.
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               ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCCGGTGGTGAGCTAATCGCCTATCTC
                                                                                                                                   TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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                                                                           GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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99US-00318528.
2000US-00580515.
2001US-00866379.
                                                                                                                                                                                                                                                                                                                                 the specification.
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the phytates.
                                                                                                                                                                                                                                                                           Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                           The present sequence encodes a phytase enzyme from Escherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate in phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli nutrition; ds.
                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 1; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                  Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112081/12
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                           CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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                                                              GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG
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AAD36473 standard; DNA; 1323 ВÞ

21-AUG-2002 (first entry)

Escherichia coli phytase DNA

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Query Match
Best Local S
Matches 1280
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                                                                                                                                                                                                                                                                                                     The patent discloses recombinant bacterial phytase from Escherichia coli CC X12 appA phytase. The enzyme has phytase activity and improved thermal CC tolerance when compared with wild-type phytase. It has improved protease CC stability at low pH. The recombinant phytase is useful for improving the CC improving the growth performance of an organism that consumes it, in CC vitro purposes related to research, discovery and development. They are CC also used for generating recombinant digestive systems, in feed treatment processes and for in CC vitro purposes related to research, discovery and development. They are CC also used for generating recombinant digestive system life forms, for CC the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of environmentally harmful chemicals that CC the reduction or possible elimination of the need for mineral CC the reduction or possible elimination of the need for mineral CC thus increasing the amount calories and nutrients present in the feed. The present sequence is a DNA encoding E. coli B phytase protein
                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; nutritional value; feed treatment process; therapy; thermal tolerance; growth performance; alcoholic drink; biopulping; non-alcoholic drink; biobleaching; B phytase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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                                                                                                                                   CAGATIGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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      ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC
                                                                                                                     CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                                                                                                                                                                      ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
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RESULT 12
ADA19445
The invention relates to an isolated Escherichia coli polynucleotide CC encoding a phytase enzyme appearing as ADA19450 and having amino acids CC modification from W68E, 084W, A95P, K97C, S168E, R180Y, N226C or Y277D. CC Also included the E. coli appa gene ADA1949 (or an oligonucleotide CC derived from it) or its mutant sequence ADA19452, expression vectors, host cells, a method of improving nutritional value of a phytate-CC containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytase in the phytate-CC containing foodstuff), a method to produce an animal feed containing a CC microbial phytase (comprising culturing the plant cell, plant part or plant under conditions where the nuclectide sequence is expressed and CC converting the plant cells, plants or plant into a composition for animal composition for animals (comprising the plant seeds, plant CC cells, plant parts or plants in admixture with a phytate-containing foodstuff), a method to treat a human or an animal able to benefit from CC comprising administering to the human or animal the plant seed, plant composition administering to the human or animal the plant seed, plant comprising administering to the human or animal the plant seed, plant comprising administering to the human or animal the plant seed, plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000; 2
                                                                                                                                                                                                                                                                                                                                Isolated Bscherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Short JM, 1
O' Donoghue
                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GARR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GRAY/)
(BART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHOR/)
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                                                                                                                                                                                                                                                                                                   2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) SHORT J M.
) KRETZ K A.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O' DONOGHUE
) MATHUR E J.
                                                                                                                                                                                                                                                                                                                                                                                                             ADA19446.
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e B, Mathu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhancement;
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; 99US-00259214.
; 99US-00291931.
; 99US-00318528.
; 2000US-00580515.
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                                                                                                                                                                                                                                                                                                  1; 62pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding phytase
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/product= "Phytase
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ur EJ;
                                                                                                                                                                                                                                                                                                  English.
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                                                            Query Match
Best Local Similarity
                                        Matches
                                                                                                                                                   cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence encoding a phytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a polypeptide having phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence encodes E. coli B wild-type phytase.
                                                                                                                       Sequence 1323
                                        1280;
                                        Conservative
                                                                                                                   BP; 323 A; 353 C; 357 G; 289 T; 0
                                                      96.7%;
98.0%;
                                        0,
                                                          Score 1265;
Pred. No. 0
                                      Mismatches
                                                                              BB
                                                                            8
                                        26;
                                                                                                                     U; 1 Other;
                                                                          Length 1323;
                                        Indels
                                        0
                                      Gaps
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문 ঠ 맑 Ş 밁 S 밁 S 8 S 밁 S Ś 밁 밁 S 밁 S 片 S 맑 ş 밁 S 밁 721 661 661 601 601 541 481 481 361 721 421 421 361 301 301 241 241 181 181 121 121 5 13 _ GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGATCACC AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC CGGCAAACGGCG AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCCTCGCATCAATGCTGACG CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC **AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT** TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG GCCTTCGCCGCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCCTAAATGTGGCCTGCCCG ACCTGGCCGGTAAAACTGGGTTGGCTGACACCCGCGNGGTGGTGAGCTAATCGCCTATCTC ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGCGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCCGCAATCTGCA CAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 780 780 720 720 660 600 600 540 540 480 480 420 420 360 180 180 360 300 120 60 60 300 240 240 120

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781

GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA

840

GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA

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RESULT 13
ADOS0291
ID ADOS0291
XX ADOS0
XX ADOS0
OT 29-JU
XX Esch
XX Phyt
XX Phyt
XX Phyt
XX PT CDS
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                                                            13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
 (SHOR/)
(KRET/)
(GRAY/)
(BART/)
                                                                                                                                                                                                                                                 unsure
                                                                                                                                                                                                                                                                                                                         Escherichia
                                                                                                                                                                                                                                                                                                                                                 Phytase; bacteria; thermal phytate; animal feed; fish
                                                                                                                                                                                                                                                                                                                                                                                                                                     AD050291;
                                                                                                                                                   20-JUN-2003;
                                                                                                                                                                                                  US2004091968-A1.
                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli B phytase
                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO50291 standard; DNA; 1323
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  SHORT J M.
KRETZ K.
GRAY K A.
BARTON N R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC
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                                                            ; 97US-00910798.
; 99US-00259214.
99US-00291931.
; 99US-00318528.
; 2000US-00580515.
; 2001US-00866379.
                                                                                                                                                                                                                                                                                                                         coli; B.
                                                                                                                                                   2003US-00601319
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                          /product= "Phytase enzyme"
214. .216
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                         note= "Encodes Arg
                                                                                                                                                                                                                                                                                                                                                                                     DNA.
                                                                                                                                                                                                                                                                                                                                               tolerance; protease stability; feed; dough; baking; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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The invention relates to a method for producing phytase that involves corporating a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow compressing the nucleic acid in a yeast under conditions that allow commercially at low ph. The phytase enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low ph. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of commercial including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, composition, higher yields and loading efficiency. The phytase composition, higher yields and loading efficiency. The phytase concorporated in to the dietary aid is safe for animals. The present of the sequence is Escherichia coli B phytase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Short JM,
Mather EJ;
                                                                                                                                                                                                                                                                                                                                                                                         Producing phytase, in encoding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-374952/35.
P-PSDB; ADOS0292.
                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                            in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GARR/) GARRETT J B
(ODON/) O'DONOGHUE
(MATH/) MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kretz K,
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de having
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ξ,
                                                                                                                                                                                                                                                                                                                                                                                             providing nucleic acid derived from bacteria phytase activity, and expressing nucleic acid
                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garrett JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O' donoghue
                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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SQ Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;

Query Match 96.7%; Score 1265; DB 12; Length 1323;

Best Local Similarity 98.0%; Pred. No. 0;

Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

— 540	481 AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT	Qy 4	
G 480	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG	Db 4	
- G 480	421 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTTGCCAACTGGATAACGCG	Qy 4	
G 420	361 GCCTTCGCCGGCGGGCGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG	Db 3	
G 420	361 GCCTTCGCCGGCCGGGCTGGCACCTGACTGCCAATAACCCGTACATACCCAGGCAGATACG	Qy 3	
A 360	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA	Db 3	
A 360	301 CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA	Qy 3	
Ġ 300	241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG	Db 2	
G 300	241 GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG	Qy 2	
C 240	181 ACCTGGCCGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC	Db 1	
C 240	181 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGGGGGGGG	Qy 1	
A 180	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA	Db 1	
A 180	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCCAGACGCATGGCCA	Qy 1	
T 120	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGG	Db	
T 120	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT	Q	
A 60	1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA	рь	
A 60	1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA	γQ	
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1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA

Query Match Best Local Sim Matches 1280;

Similarity

96.7%; ilarity 98.0%; Conservative

Score 1265; I Pred. No. 0; 0; Mismatches

DΒ

12; 26;

Length 1323; Indels

0

Gaps

<u>,</u>

Sequence 1323

BP; 325

A; 353

C; 356 G; 288 T;

0 U;

1 Other,

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CC The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC improves animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present Sequence is Kangaroo rat Escherichia coli phytase mutant DNA. Note: The present sequence is not shown in the specification but has been derived cover.
                                                                                                                                                                                                                                                                                                                                                                                                            Short JM,
Mather EJ;
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25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                  Disclosure; Page; 74pp; English.
                                                                                                                                                                                                                                                                                                                          Producing phytase, involves encoding polypeptide having
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(KRET/)
(GRAY/)
(BART/)
(GARR/)
(ODON/)
(MATH/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE B
) MATHER E J.
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99US-00291931.
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                                        TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
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CGTCGGCTAAGCGATAACAGCCAGTGGATTCCAGGTTTTCGCTGGTCTTCCAGACTTTTACAG
                                                                                                                          TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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                                                                                                      TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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Producing phytase, involves providing nucleic acid derived

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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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Mather EJ;
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P-PSDB; ADO50292, ADO50304.
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) KRETZ K.
) GRATON N R.
) GARRETT J B.
) O'DONOGHUE E.
) MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteria; thermal tolerance; protease stability; foodstuff; animal feed; fish feed; dough; baking; mutant; gene; ds.
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2001US-00866379.
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The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC commercially significant mammals such as pigs, goats, laboratory rodents, commercially CC significant mammals such as sigs, goats, laboratory rodents, commercially CC expression of the such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in distary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present sequence is Escherichia coll M phytase mutant DNA. Note: The present CC sequence is not shown in the specification but has been derived from Escherichia coll B phytase DNA ADO50291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1280; Conserv
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                     CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                                    CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                            TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                                                                               AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGGCTTTACCGGGCAT
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ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC 1306	ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC 1306	CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	CTGGCAGGATGTGAAGAGCGAAAATGCGCAGGGCATGTGTTCGTTTGGCAGGTTTTTACGCAA 1260	CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC 1200	CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAAGAGGTGAAACTGACC 1200	CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTTACAG 1140	ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020	TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020	TIGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTACTG 960	TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCCACTTCAGTGCTG 960	CGCACGCCAGAGGTTGCCCCGCAGCCCGCGCCCCCGTTATTGGATTTGATCAAGACAGCG 900	CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCCGTTATTAGATTTGATCAAGACAGCG 900	GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840	GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA 840	GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACC 780	GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC 780	AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGGGGTAAGCCTCGCATCAATGCTGACG 720

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Listing first 45 summaries
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     GenEmbl:*
1: gb env:
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11432.839 Million cell updates/sec
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AR127918

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3	B & B &	B & B &	RESULT 1 AR108133 LOCUS DEFINITIO ACCESSION VERSION KEYWORDS SOURCE ORGANIS REFERENCE AUTHORS TITLE JOURNAL FEATURES BOUR ORIGIN ORIGIN Query M Gest Lo Matches	D + 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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                         AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                              GAGATATTTCTCCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTTGGGGAAGGATCACC
                                                  AACGTGACTGACGCGATCCTCGAGAGGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                                                         AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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AR127818
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Best Local Similarity
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M Unclassified.

B 1 (bases 1 to 1323)

S Short, J.M. and Kretz, K.A.

Recombinant bacterial phytases and use Patent: US 6183740-A 1 06-FEB-2001;
Location/Qualifiers

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                                                  GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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Ouery Match 96.7%; Score 1265; DB 2; Length 1323; Best Local Similarity 98.0%; Pred. No. 0; Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0; Oy 1 ATGANAGCGATCTTANTCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	S Unknown. ISM Unknown. Unclassified. Unclassified. El (bases 1 to 1323) SKretz,K. Phytase Location/Qu Irce /mol_type="""	RESULT 3 AR130956 LOCUS AR130956 DEFINITION Sequence 1 from patent US 6190897. ACCESSION AR130956 VERSION AR130956.1 GI:14119281	QY 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGATCTCATC 1306	QY 1201 CTGGCAGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260	QY 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1200	Qy 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG 1140	Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	Oy 961 TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCGCACTGGAGCTCAACTGG 1020	OY 901 TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 960	Qy 841 CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG 900	Qy 781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA 840	Db 721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780
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Best Local Similarity 98.0%;
Matches 1280; Conservative
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Short.J.M. and Kretz,K.A.
Phytase-containing foodstuffs and methods
Patent: US 6720014-A 1 13-APR-2004;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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Short,J.M., Kretz,K.A., Gray,K.A., Ba Short,J.M., Kretz,K.A., Gray,K.A., Ba O'Donoghue,B. and Mathur,E.J.
Recombinant bacterial phytases and us Patent: US 685365-A 1 15-FEB-2005; Patent: US 685365-A 1 15-FEB-2005; Diversa Corporation, San Diego, CA Location/Qualifiers

1. 1323
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Sequence
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                              ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
                                                                                                   TTTATTGCCGGACACGATACTAATCTGGCAAATCTCGGCGCGCACTGGAGCTCAACTGG
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Bacteria, Proteobacteria, Gammaproteobacteria,
Enterobacteriaceae, Escherichia.
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Enterobacteriaceae; Escherichia.
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Matches 1280; Conserv 301 181 361 301 241 241 181 121 121 61 61 GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG ACCTGGCCGGTAAAACTGGGTGAGCTGACCACCGCGGGGGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTTTGATTCCGTTAACCCCGCAATCTGCA CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA Conservative 96.7%; Score 1265; Di Pred. No. 0; 0; Mismatches 0, DB 2; 26; Length 0,

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TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG

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Bacteria; Proteobacteria; Gammaproteobacteria;
Bacteria; Escherichia.
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Sequence 1 from Patent WO0190333.
AX356566
Recombinant bacterial phytases and uses Patent: WO 0190333-A 1 29-NOV-2001;
                                       Short, J.M., Kretz, K.A., Gray, K.A.,
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ilarity 98.0%;
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PPGGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSLRSHHHHHHH"
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Query Match 96.6%; Score 1263.8; DB 2; Length 1901; Best Local Similarity 98.2%; Pred. No. 0; Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0; Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0; Qy 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 60	FEATURES Location(Qualifiers 11901 /organism="unknown" /mol_type="genomic DNA" ORIGIN	AUTHORS Short, J.M., Kretz, K.A., Gray, K.A., Barton, N.R., Garrett, J.B., O'Donoghue, E. and Mathur, E.J. TITLE Recombinant bacterial phytases and uses thereof JOURNAL Patent: US 6855365-A 6 15-FEB-2005; Diversa Corporation: San Diego, CA	Unknown. M Unknown. Unclassified. 1 (bases 1 to 1901)	AR636199 AR636189 1901 bp DNA linear PAT 20-APR-2005 DEFINITION Sequence 6 from patent US 6855365. ACCESSION AR636189 VERSION AR636189 AR636189.1 GI:62768872 KEYWORDS .	Db 42299 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGTAAT 42338 RESULT 11	126	AGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1	OY 1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAGAGGGTGAAACTGACC 1200	QY 1081 CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1140	OY 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG 1080	OY 961 TITATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG 1020	Qy 901 TIGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGAGACATTACCCACTTCAGTGCTG 960	QY 841 CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG 900	Qy 781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA 840	OY 721 GAGATATTTCTCCTGCAACAAGCACAGGGAATCGCGGAGCCGGGGTGGGGAAGGATCACC 780	41699 AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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Short, J.M., Kretz,K.A., Gray,K.A., Barton,N.R.,
O'Donoghue,B. and Mathur,E.J.
Recombinant bacterial phytases and uses thereof
Patent: US 685365-A 7 15-FEB-2005;
Diversa Corporation; San Diego, CA
Location/Qualifiers
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                                               Short, J.M., Kr
O'Donoghue, E.
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Bacteria; Proteobacteria; Gammaproteobacteria;
             Recombinant bacterial phytases and Patent: WO 0190333-A 6 29-NOV-2001; DIVERSA CORPORATION (US)
                                                                                         Enterobacteriaceae; Escherichia
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 Location/Qualifiers
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                                                              Kretz, K.A., Gray, K.A.,
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                                                                  Garrett, J.B.
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Similarity 98.2%;
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/mol_type="unassigned I
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Recombinant bacterial phytases and uses
Patent: WO 0190333-A 7 29-NOV-2001;
DIVERSA CORPORATION (US)
Location/Qualifiers
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Sequence
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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             GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG
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GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG
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                                                                                                                 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
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J. Bic
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The complete nucleotide sequence of the reveals significant homology between pH glucose-1-phosphatase
J. Bacteriol. 172 (9), 5497-5500 (1990)
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Asp304 of Escherichia coli acid phosphatase
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1 (bases 1 to 1901)
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NVTDAILSRAGGSIADPTGHRQTAFRELERVLMFPGSMGRITDSHQMVTLLSLHNAQF
YLLQRTPEVARSRATPLLDLIKTALTPHPPQKGAYGVTLPTSVLFIAGHTTNLANLGG
ALELWTLPGQPDNTPPGGELVFERRRELSNNSQWIQVSLVFQTLQOMRDKTPLSLNT
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               PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL"
188. .253
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133. .138
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88. .1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MWYLLWFVGILLMCSLSTLVLVWLDPRLKS"
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Similarity 98.2%;
77; Conservative
                                       CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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299. .301
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299. .301
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note="created by site directed mutagenesis"
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CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 1260 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG CGCACGCCAGAGGCTTGCCCGCAGCCGCCCACCCCCGTTATTAGATTTGATCAAGACAGCG GATTCACACCAGTGGAACACCTTGCTAAGTTTTGCATAACGCGCAATTTTATTTGCTACAA GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGGGGCCGGGGTGGGGAAGGATCACC AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC AACGTGACTGACGCGATCCTCGAGAGGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG TTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACACTTTACCCCACTTCAGTGCTG **AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG** CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG 1487 1087 1080 1207 1020 1147 1027 840 1387 1200 1327 1140 960 900 780 907 720 847 660 787 600 727 540 667 480 607 967

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Post-processing: Minimum Match 0%
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*

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10: /EMC_Celerra_SIDS3/ptodata/2/ina/Ba_COMB.seq:*
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US-09-866-379-9
US-09-866-379-9
US-09-715-477-2
US-09-715-477-4
US-09-715-477-4
US-09-715-798-1
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US-09-621-976-15639
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
16384, A	1, Appli	3732, Ap	12755, A	94, Appl	20, Appl	1, Appli	1286, Ap	 Appli 	16326, A	14187, A	17, Appl	17, Appl	17, Appl	116, App	1, Appli	8976, Ap	14757, A	5, Appli	109217,	109216,	109215,

ALIGNMENTS

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US-09-259-214-1

Sequence 1, Application US/09259214A

Patent No. 6110719

GENERAL INFORMATION:
APPLICANT: Kretz, Keith
FILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVER1370-1

CURRENT APPLICATION NUMBER: US/09/259,214A

CURRENT APPLICATION NUMBER: 08/910,798

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER APPLICATION SUMBER: 08/910,798

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER APPLICATION NUMBER: 08/910,798
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Bscherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or
US-09-259-214-1
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Best Local S
Matches 1280
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| Sequence 1, Application Us/09318528
| Patent No. 6183740
| GENERAL INFORMATION:
| APPLICANT: Kretz, Keith
| TITLE OF INVENTION: NOVEL PHYTASE
| FILE REFERENCE: 09010/029003
| CURRENT APPLICATION NUMBER: Us/09/318,528
| CURRENT PILING DATE: 1999-05-25
| EARLIER APPLICATION NUMBER: 09/291,931
| EARLIER FILING DATE: 1999-04-13
| EARLIER FILING DATE: 1999-08-13
| EARLIER FILING DATE: 1999-03-01
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FRESEQ FOR Windows Version 4.0
| SEQ ID NO 1
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; ORGANISM: Escherichia co
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; NAME/KEY: misc feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A
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GENERAL INFORMATION:
APPLICANT: Kretz, Keith
ITILE OF INVENTION: NOVEL PHYTASE
ITILE OF INVENTION: NOVEL PHYTASE
ITILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
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APPLICANT: GARTY, Nelson

APPLICANT: BARTON, Nelson

APPLICANT: O'DONOGHUE, Eileen

ITITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/518,528

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR APPLICATION NUMBER: US 09/21,931

PRIOR RILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 09/259,214

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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
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Best Local Similarity 98.0%;
Matches 1280; Conservative
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RESULT 6
US-09-866-379-6
US-09-866-379-6
; Sequence 6, Application US/09866379
; Patent No. 685365
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: KRETZ, Keith
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SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 1901

TYPE: DNA

ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (1901)

OTHER INFORMATION: n is any nucleotide
US-09-866-379-6
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APPLICANT: BARTON, Nelson
APPLICANT: GARREIT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHY
TITLE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/297,931
PRIOR APPLICATION NUMBER: US 09/299,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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                  ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTGAGAT 1300
                                                                             CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTTACGCAA 1260
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US-09-866-379-7
; Sequence 7, Application US/09866379
; Patent No. 6855365
; GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
; CURRENT APPLICATION NUMBER: US/09/866,379
; CURRENT APPLICATION NUMBER: US/09/866,379
; CURRENT APPLICATION NUMBER: US/09/866,379
; PRIOR APPLICATION NUMBER: US/09/866,379
; PRIOR FILING DATE: 1090-05-25
; PRIOR APPLICATION NUMBER: US 09/318,528
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: US 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: US 09/259,214

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; ERATURE:
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; LCCATION: (1)...(1901)
; OTHER INFORMATION: n is any nucleotide
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PRIOR APPLICATION NUMBER: US 01
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
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Best Local Similarity 98.2
Matches 1277; Conservative
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GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA
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98.2%; Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
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US-09-866-379-5
; Sequence 5, Application US/09866379
; Patent No. 6855365
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APPLICANT: BARRON, Nelson
APPLICANT: GARRON, Helson
APPLICANT: GARRETT, James
APPLICANT: GO'DONOGHUE, E11een
ITILE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1901)
US-09-866-379-5

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ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
                                                                                                                                                  CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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Pred. No. 0;
0; Mismatches
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Sequence 9, Application US/09866379

Patent No. 685356

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: SHORT, Jay

APPLICANT: GRAY, Kevin

APPLICANT: GRAY, Kevin

APPLICANT: GARRETT, James

APPLICANT: GODNOGHUS, Eileen

TITLE OP INVENTION: RECOMBINANT BACTERIAL PHYTASES AND

FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US/09/80,515

PRIOR APPLICATION NUMBER: US/09/80,515

PRIOR FILING DATE: 1090-05-25

PRIOR APPLICATION NUMBER: US/09/318,528

PRIOR APPLICATION NUMBER: US/09/318,528

PRIOR APPLICATION NUMBER: US/09/291,931

PRIOR APPLICATION NUMBER: US/09/29,214

PRIOR APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Escherichia coli; FEATURE; ; NAME/KEY: misc feature; LOCATION: (1)..(1901); OTHER INFORMATION: n is any nucleotide US-09-866-379-9
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                                                                                                                                            TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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Pred. No. 0;
0; Mismatches
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; Sequence 2, Application US/09715477
; Patent NO. 6841370
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
; FILE REFERENCE: 19603/4031
; CURRENT APPLICATION NUMBER: US/09/715,477
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,179
; PRIOR APPLICATION NUMBER: 09/11-18
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-715-477-2
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Best Local Similarity
Matches 1257; Conserv
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                CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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                                                                                    TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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nilarity 97.0%;
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RESULT 11 US-09-540-149A-9 ; Sequence 9, Application US/09540149A Patent No. 6511699 ; GENERAL INFORMATION: APPLICANT: Lei, Xingen TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY FILE REFERENCE: 19603/2791 ; CURRENT APPLICATION NUMBER: 60/127,032 PRIOR APPLICATION NUMBER: 60/127,032 PRIOR FILING DATE: 1999-03-31 ; NUMBER OF SEQ ID NOS: 9 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 9 ; LENGTH: 1489 ; SEQ ID NO 9 ; LENGTH: 1489 ; ORGANISM: Escherichia coli US-09-540-149A-9 Query Match Best Local Similarity 96.5%; Pred. No. 0; Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps Qy 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTTTGATTCCGTTAACCCCGCAATCTGCA 1	Db 1388 CTGGCAGGATGTGAAGAGCGAAATGCGGCAGGGCATGTGTTCGTTGGCCGGTTTTACGCAA Qy 1261 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1296 Db 1448 ATCGTGAATGAAGCGCGCATACCGGCGTGCAGTTTG 1483	1141 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC	Qy 1021 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG		841 CGCACGCCAGAGGTTGCCCGCAGCCGCGCACCCCCGTTATTAGATTTGATCAAGACAGCG	QY 781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA	Qy 721 GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACCC	QY 661 AAGGTGAGCGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
0; 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,	1447 Db Oy Oy Db		1080 Qy 1267 pb 1140 Qy 1327 pb	1147 DB 11020 QY 1207 Db		840 Qy 1027 Db	780 Qy 967 Db	720 Qy 907 Db
721 GAGATATTTCTCCTGCAACAAGCACAGGAATGCCCGGAGCCGGGGTGGGGAAGGATCACC 780	782 CTTAACCGTGAGAAAACAGGAAGGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 841 661 AAGGTGAGGCCGACTGTGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG 720	541 TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC 600	421 TCCAGTCCCGATCCGTTATTAATCCTCTAAAACTGGCGTTTGCCAACTGGATAACGCG 480		4 4 0 0	181 ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGGGTGGTGAGCTAATCGCCTATCTC 240	121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180	61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120

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GENERAL INFORMATION:

APPLICANT: Lei, Xingen
TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVED PHYTASE ACT
FILE REFERENCE: 19603/2798
CURRENT APPLICATION NUMBER: US/10/266,041A
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9
LENGTH: 1489
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Best Local Similarity 96.5%;
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                    AACGTGACTGACGCGATCCTCGAGAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT 540
                                                                                                                                        GCCTTCGCCGGGCTGGCACCCTGACTGTGCAATAACCGTACATACCCCAGGCAGATACG
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                                                                                                                                                                                  CAGCCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAAACAGGCGAA
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Pred. No. 0;
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                                                                               GENERAL INFORMATION:
APPLICANT: Lei, Xingen
ITITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
FILE REFERENCE: 19603/4031
CURRENT PILING DATE: 19603/90/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-715-477-4
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                                                                                                                               US-08-910-798-1
                                                                                                                                                                                                                                                       TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                               Query Match 88.1
Best Local Similarity 94.1
Matches 1229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application Patent No. 5876997
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KRETZ
TITLE OF INVENTION: NOVEL PHYTASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suit
CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US

ZOUNTRY: US

ZOUNT : 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, VG

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                         MOLECULE TYPE: DN
IMMEDIATE SOURCE:
CLONE: PHYTASE
PEATURE:
                                                                                                                                            NAME/KEY:
LOCATION:
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                                                             Score 1153;
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RESULT 15

US-09-489-039A-341

Sequence 341, Application US/09489039A

Patent No. 6610336

GENERAL IMPORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT APPLICATION MIMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR FILLING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 341

LENGTH: 1266

TYPE: DNA

ORGANISM: Klebsiella pneumoniae
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                            CTGACTGTGCAATAACCGTACATACCCAGGCAGATACGTCCAGTCCCGATCCGTTATTTA
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ACCCGGTTATTACCGACGACTCCCCGGCGTTTCGCGAGAAAGCGCTGCAGGCGAT
                                                            CGGGCTGCGGCATCCCGGTGCATCACCAGCCTCAGATGGGCACCATGGACCCGACCTTCA
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-98-66-379-8
US-10-156-660-4
US-10-156-660-4
US-10-156-379-8
US-10-156-354-4
US-11-056-354-4
US-11-056-354-4
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US-11-056-354-1
US-10-284-962-1
US-10-156-660-2
US-10-051-319-10
US-11-056-354-2
US-10-031-723A-16
US-09-866-379-10
US-11-074-522-12
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195	195	195	326	412.5	472.5	476.5	611.5	657	760	932.5	935.5	943.5	960.5	1203	2066	2066	2070
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US-10-450-763-53707	US-10-343-357-6	US-10-257-174-44	US-10-450-763-56055	US-11-098-686-10683	US-10-021-723A-6	US-10-021-723A-8	US-10-021-723A-14	US-10-450-763-54615	US-10-021-723A-10	US-10-021-723A-4	US-10-021-723A-2	US-10-282-122A-77792	US-10-021-723A-12	US-10-450-763-56057	US-10-021-723A-15	US-10-021-723A-13	US-10-334-671-1
Sequence 53707, A	Sequence 6, Appli	Sequence 44, Appl	Sequence 56055, A	Seguence 10683, A	Sequence 6, Appli	Sequence 8, Appli	Sequence 14, Appl		Sequence 10, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 77792, A	Sequence 12, Appl	0	Sequence 15, Appl	Sequence 13, Appl	Sequence 1, Appli

ALIGNMENTS

US-09-777-566A-2

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Sequence 2. Application US/09777566A

Patent No. US20010055788A1

PATENTAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: SHORT, Jay

APPLICANT: SHORT, Jay

PILE REFERENCE: DIVER1370-6

CURRENT APPLICATION NUMBER: US/09/777,566A

CURRENT FILING DATE: 2001-06-11

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR PILLING DATE: 1999-05-25

PRIOR FILLING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR PILLING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 4

SOPPMEABER OF SEQ ID NOS: 4

SOPPMEABER: US OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                            / Match 100.0%; Score 2302; DB 3; Local Similarity 100.0%; Pred. No. 2.2e-193; Les 440; Conservative 0; Mismatches 0;
181 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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                                                                                                 121 AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
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APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLS OF INVEXTION: RECOMBINANT BACTERIAL PHYTASES AND USES THERBOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PRILING DATE: 1000-05-25
PRIOR PILING DATE: 1000-05-25
PRIOR PILING DATE: 1000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09866379
Patent No. US20020136754A1
; GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
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Best Local Similarity
Matches 440; Conserv
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                         RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
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APPLICANT: K-etz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CUURRENT APPLICATION UNMER: US/10/034,985
CUURRENT APPLICATION UNMER: US/09/580,515
PRIOR APPLICATION UNMER: US/09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION UNMER: 09/291,931
PRIOR APPLICATION UNMER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR PRIOR PRIOR DATE: 1997-08-13
PRIOR PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ FOR Windows Version 4.0
SEQ ID NO 2
LENGTH: 440
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Publication No. US20030049815A1
GENERAL INFORMATION:
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Best Local Similarity
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RRLSDNSQWIQVSLVFQTIQQMRDKTFLSLNTFPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                          LTPHPPQKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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APPLICANT: K-ett,
FILLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/10/430,356
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US/980,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
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US-10-430-356-2
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US-10-430-356-2
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Best Local Similarity 100.0%;
Matches 440; Conservative 0
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                                                IVNEARIPACSLRSHHHHHH 440
                                                                                                       RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 2.2e-193;
Nismatches 0; Indels 0
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SEQ ID NO 2
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IVNEARIPACSLRSHHHHHH
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RESULT

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APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND MET
TITLE OF INVENTION: RECOMBINANT PHYTASES AND MET
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,931
PRIOR APPLICATION NUMBER: US 09/29,791
PRIOR APPLICATION NUMBER: US 09/29,793
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 199-08-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-13
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Best Local Similarity 100.0%;
Matches 440; Conservative 0
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
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ORGANISM: Escherichia
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                                IVNEARIPACSLRSHHHHHH 440
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Pred. No. 2.2e-193;
0; Mismatches 0;
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US-10-933-115-2

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SOFTWARE: PASKSEQ for Windows Version
SEQ ID NO 2
LENGTH: 440
TYPE: PAT
ORGANISM: Escherichia coli
US-10-933-115-2
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CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR PILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/299,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 10 NOS. 10
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
TILE REFERENCE: 564462001822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 440; Conserv
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                                     IVNEARIPACSLRSHHHHHH 440
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APPLICANT: O'DONOGHO, Elleen
FILTE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USE
FILTE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USE
FILTE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USE
FILTE OF INVENTION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1997-08-13
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Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Melson
APPLICANT: GARRETT, James
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US-09-866-379-8
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Best Local Similarity
Matches 430; Conserv
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IVNEARIPACSL 432
                                                                          RRLSDNSQWIQVSLVFQTLQQMRDXTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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99.5%;
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Pred. No. 1.7e-187;
0; Mismatches 2;
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FILE OF INVENTION: AND PROPERTY OF THE REFERENCE: 09010-029007

CURRENT APPLICATION NUMBER: US/10/156,660

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

VOMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 432

TYPE: PRT

ORGANISM: Escherichia coli
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Best Local Similarity 99...
430; Conservative
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APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
APPLICANT: Garrett, Jamee
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TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS
TITLE OF INVENTION: AND METHODS FOR MAKING
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IVNEARIPACSL 432
                         IVNEARIPACSL 432
                                                                      RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                            RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.1%; Score 2235; DB 4; Length 432; 99.5%; Pred. No. 1.7e-187; tive 0; Mismatches 2; Indels
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APPLICANT: CAIL, USCALLA
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Gen
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/246,578
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
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US-10-282-122A-43351
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US-10-282-122A-43351
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SEQ ID NO 43351
LENGTH: 432
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Mang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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APPLICANT:
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Local Similarity 99.5%;
Les 430; Conservative
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EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA 300
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2235; DB 4; Length 432;
Pred. No. 1.7e-187;
0; Mismatches 2; Indels
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APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
APPLICANT: O' Donoghue, Eileen
APPLICANT: O' INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 1909-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-05-05
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1997-08-13
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US-10-601-319-8
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LENGTH: 432
TYPE: PRT
ORGANISM: Escherichia
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Publication No. US20040091968A1
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                                                        RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
                                                                           RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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GENERAL INFORMATION:

APPLICANT: Cargill, Incorporated
TITLE OF INVENTION: Myo-Inositol Oxygenases
FILE REFERENCE: 10829/003US1
CURRENT APPLICATION NUMBER: US/10/472,317
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PAID PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEG ID NOS: 72
SOPTWARE: PASTSEQ for Windows Version 4.0
SEG ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia US-10-472-317-41
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US-10-472-317-41
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Best Local Similarity
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                                 IVNEARIPACSL 432
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Pred. No. 1.7e-187;
0; Mismatches 2;
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RESULT 12 US-10-933-115-8

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PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 432
TYPE: PRT
ORGANISM: Escherichia coli
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Publication No. US20050281792A1
GENERAL INFORMATION:
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Best Local Similarity 99.5
Matches 430; Conservative
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
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Garrett, James B.
O' Donoghue, Eileen
Mathur, Eric J.
IVNEARIPACSL 432
                              IVNEARIPACSL 432
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APPLICANT: GARRET, NOVILLA:
APPLICANT: GARRET, James B.
APPLICANT: O'DONOCHUE, Sileen
APPLICANT: O'DONOCHUE, Sileen
APPLICANT: O'DONOCHUE, Sileen
APPLICANT: MATHUR, ERIC J.
ITITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM AND METHODS
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
FILE REFERENCE: 564462001803/D1370-9C1
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT APPLICATION NUMBER: US/11/056,354
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-08-13
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Publication No. US20050246780A1
GENERAL INFORMATION:
APPLICANT: SHORT, Jay M.
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin A.
APPLICANT: BARTON, Nelson R.
APPLICANT: GARRETT, James B.
APPLICANT: GARRETT, James B.
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; ORGANISM: Escherichia coli appA phytase
US-11-056-354-4
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SOFTWARE: PatentIn version
SEQ ID NO 4
LENGTH: 432
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Best Local Similarity 99.5%;
Matches 430; Conservative
                         361 RRLSDNSQWIQVSLVFQTLQQMRDKTFLSLNTPPGGVKLTLAGCEERNAQGMCSLAGFTQ 420
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RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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Pred. No. 1.7e-187;
D; Mismatches 2;
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Sequence 1, Application US/11018709
Publication No. US2005095691A1
GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/11/018,709
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: US/99/715,477
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR PHILING DATE: 2001-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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US-10-284-962-3
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; LENGTH: 432
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-018-709-1
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US-11-018-709-1
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Sequence 3, Application US/10284962
Publication No. US20030206913A1
GENERAL INFORMATION:
APPLICANT: Webel, Douglas M.
APPLICANT: Orr, Donald E.
APPLICANT: Ruch, Frank E.
APPLICANT: Ruch, Frank E.
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Best Local
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Similarity 99.3%;
29; Conservative
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Pred. No. 4.6e-187;
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FILE REFERENCE: 834460-71725
CURRENT APPLICATION NUMBER: US/10/284,962
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/335,303
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 432
LENGTH: 432
TYPE: PRT
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US-10-284-962-3
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Best Local Similarity 99.1%;
Matches 428; Conservative
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Pred. No. 2.8e-186;
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Search completed: June 13, Job time: 145.303 secs 2006, 10:50:37

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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seq length: 2000000000
Query
Match
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1: /EMC_Celerra_SIDS3/ptodata/2/laa/5_COMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/laa/6_COMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/laa/7_COMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/laa/H_COMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/laa/PCTUS_COMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/laa/RE_COMB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/2/laa/RE_COMB.pep:*
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US-10-266-041A-1
US-09-540-149A-1
US-09-866-379-10
US-09-866-379-10
US-09-489-039A-7512
US-09-489-039A-7512
US-09-489-039A-13501
US-09-684-855-128
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US-09-259-214-2
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27
111	114.5	114.5	117	117	117	117	117	117	117	118	118	118	118	119	119	119	119	119
. 8	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.2	5.2	5.2	5.2	5.2
440	585	326	515	515	515	386	386	386	386	440	440	440	440	465	465	465	465	465
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US-09-684-855-108	US-10-144-678A-1020	US-09-270-767-41623	US-09-344-195-2	US-08-579-823A-2	US-09-146-283-2	US-09-949-016-6022	US-09-097-199-48	US-08-692-787-48	US-08-758-213-1	US-09-488-265B-7	US-09-684-855-152	US-09-684-855-129	US-09-684-855-107	US-10-229-358-6	US-10-062-848-78	US-09-635-504-33	US-10-083-452-8	US-09-273-871A-8
Sequence 108, App	Sequence 1020, Ap	Sequence 41623, A	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6022, Ap	Sequence 48, Appl	Sequence 48, Appl	Sequence 1, Appli	Sequence 7, Appli	Sequence 152, App	Sequence 129, App	Sequence 107, App	Sequence 6, Appli	Sequence 78, Appl	Sequence 33, Appl	Sequence 8, Appli	Sequence 8, Appli

ALIGNMENTS

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RESULT 1

US-09-259-214-2

; Sequence 2, Application US/09259214A

; Patent No. 6110719
; GENERAL INFORMATION:

; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: DIVER1370-1
; CURRENT APPLICATION NUMBER: US/09/259,214A
; CURRENT FILING DATE: 1999-03-01
; EARLIER APPLICATION NUMBER: 08/910,798
; EARLIER FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-259-214-2
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	Query Match Best Local Similarity Matches 440; Conser	tch 100.0%; Score 2302; DB 2; Length 440; al Similarity 100.0%; Pred. No. 3.9e-234; 440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ş	,	MKAILIPELSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60
g	<u> </u>	MKAILIPPLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60
ક	, 61	TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
뭥	61	TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
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뮻	121	AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
Ş	, 181	RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
밁	181	SLTQALPS
5	241	BIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300
日	241	EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300
S	301	LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
문	301	LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
ठ	361	RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420

Length 440; Indels

0;

Gaps

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; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Escherichia c
US-09-318-528-2
   RESULT 3
US-09-291-931-2
; Sequence 2, Application US/09291931A
; Patent No. 6190897
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Best Local
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CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-03-01
EARLIER FILING DATE: 1999-03-01
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TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
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SOFTWARE: PastSEQ for Windows Version
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Pred. No. 3.9e-234;
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APPLICANT: Kretz, Keith
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/02903
CURRENT FILING DATE: 1999-04-13
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Escherichia
US-09-291-931-2
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APPLICANT: KFetz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/580,51
CURRENT FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
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                                                                                                                                                                                                                                                       Sequence 2, Application US/09580515 Patent No. 6720014
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Pred. No. 3.9e-234;
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420

360 300 300 240

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180 180 120 120 60

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Sequence 2, Application US/09866379
Patent No. 6855365
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
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US-09-866-379-2
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; ORGANISM: Escherichia
US-09-580-515-2
             FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/292,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 440
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APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Elleen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
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Local Similarity 100.0%;
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PatentIn version 3.1
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; LENGTH: 440
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Best Local Similarity 100.0%;
Matches 440; Conservative (
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           IVNEARIPACSLRSHHHHHH 440
                                                             RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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IVNEAR I PACSLRSHHHHHH
                                             RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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                                                                                            LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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Pred. No. 3.9e-234;
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US-09-866-379-8

US-09-866-379-8

Sequence 8, Application US/09866379

Patent No. 6855365

GENERAL INFORMATION:
APPLICANT: INFORMATION
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: HARTON, Nelson
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: O'DONOGHUE, Elileen
ITILE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/291,931

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RESULT 7
US-09-715-477-1
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; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-715-477-1
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE
FILE REFERENCE: 1960/4031
CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1992-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09715477 Patent No. 6841370
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Best Local Similarity 99.5%;
                                                                                                                       Matches 429;
                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                              SEQ ID NO 1
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                                                                                                                                      Local Similarity
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               TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
                                                         MKAILIPPLSLLIPLTPQSAPAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60
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                                                                                                                   Score 2230; DB 2;
Pred. No. 1.5e-226;
0; Mismatches 3;
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Pred. No. 4.5e-227;
                                                                                                                                                   Length 432;
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; Sequence 1, Application US/10266041A
; Patent No. 6974690
; GENERAL INFORMATION:
APPLICANT: Lei, Xingen
TITLE OF INVENTION: PHOSPHATASESS WITH IMPROVED PHY
FILE REFERENCE: 19603/2798
; CURRENT APPLICATION NUMBER: US/10/266,041A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/127,032
; PRIOR FILING DATE: 1999-03-31
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 09/540,149
; PRIOR APPLICATION NUMBER: 09/540,149
; PRIOR PILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
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Best Local Similarity
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TYPE: PRT
ORGANISM: Escherichia
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Pred. No. 1.4e-225;
0; Mismatches 4;
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; LOCATION: (433)
; OTHER INFORMATION: Xaa at position 433 in this sequence is unknown
US-09-540-149A-1
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US-09-540-149A-1
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Matches 428;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 1960/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Escherichia
FEATURE:
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IVNEARIPACSL 432
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Pred. No. 1.4e-225;
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RESULT 10

RESULT 11 US-08-910-798-2

; Sequence 2, Application U
; Patent No. 5876997
; GENERAL INFORMATION:
APPLICANT: KRETZ
; TITLE OF INVENTION: NUMBER OF SEQUENCES:

NOVEL

US/08910798

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
SIRRET: 4225 Executive Square, St

Suite 1400

CITY: La Jolla STATE: California COUNTRY: US

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

ZIP: 92037

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CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 432
TYPE: PRT
RORANISM: Escherichia coli
US-09-715-477-3
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APPLICANT: Lei, Xingen
TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE
FILE REFERENCE: 19603/4031
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Best Local (
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Local Similarity 98.6%;
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IVNEARIPACSL
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Pred. No. 2e-224;
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US-08-910-798-2
       GENERAL INFORMATION:
APPLICANT: BIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: KRETZ, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GRARETT, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
                                                                                                                                                                  Sequence 10, Application US/09866379
Patent No. 6855365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 423;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
REFERENCE: DIVER1370-7
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96.1%;
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Pred. No. 8.3e-223;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN OF SEQ ID NOS: 10
LENGTH: 430
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US-09-489-039A-7512
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GENERAL INFORMATION:
APPLICANT: GAIY BREGON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                         Sequence 7512, Application US/09489039A
Patent No. 6610836
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Best Local Similarity
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 3.9e-217;
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RESULT 14
US-09-489-039A-13501
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 13501 LENGTH: 522
                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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Best Local Similarity 32.1
Matches 134; Conservative
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LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FITLE OF INVENTION: PREUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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ORGANISM: Klebsiella pneumoniae
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120 EAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTG
                                                                           164 TEWTTHDGELTGHGYAAVVNKGRAEGOHYROLGIL-QAGCPTAESIYVRASPLORTRATA
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                                                                                                                                                                           GGLURLFIACALFLIALQSAAA---ADWQLEKVVELSRHGIRFFTAGNREAIBAATGRFW
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                                                                                                                          PTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09489039F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- AKVTLLVGHDSNIASLLTALDFKPYQLPGQYERTPIGGKLLFQRWHDSAGNRD
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; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3
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APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: MODIFIED PHYTASES
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
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SOFTWARE: PatentIn Ver.
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 QALVDGAFPGCGVAIHYV--SGDADPLFQTDKFAATQTDPARQLAAVKEKAG----DLAQ 276
                                                                                                                                                                                                                                                                                                                                                  83 KGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVP-----FIR 132
                                                                                                                                                                                                                                                                                                                                                                                                   59 -----WPTWPVKLGW--LTPRGGELIAYLG--HYQRQRLVADGLLAKKGCPQSGQVAII 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 PFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPT----KATQLMQDVTPDA---
  HNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQ-----AYGVTLPTSVLFIA 323
                                                    DEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNE------W-----KKYNYLQSL 271
                                                                                                                                                                                           CQLDNANVTDAILSRAGGSI-ADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLT 213
                                                                                                  QALPSEL--KVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL 271
                                                                                                                                                                                                                                                 ASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVII-PESETFN-----NTLDHGV
                                                                                                                                                                                                                                                                                                   ADVDERTRKTGEAFAAGL------APDCAITVHTQADTSSPDPLFNPLKTGV 154
                                                                                                                                                    C-----TKFEASQLGDEVAANFT------ALFAP--DIRARAEKHLPGVTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFFSLEDELSVSSKLPK---DCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG-QPDNTPPGGELV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCPFQAAITALGQRIDRSSAPAVAM 519
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TOMSCHY, Andrea
van LOON, Adolphus
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Result
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-MODEL=frame+ p2n.model -DEV=xlp
-Q-/abse/ABSSWEB spool/USI0601319/runat 12062006 180052 27516/app_query.fasta_1
-Q-/abse/ABSSWEB spool/USI0601319/runat 12062006 180052 27516/app_query.fasta_1
-DB=EST QFMT=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORR=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abse03p
-USER-USI0601319 @CGN 1 12067 @runat 12062006 180052 77516 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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. 7401.587 Million cell updates/sec
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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ALIGNMENTS

	TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BJ074127/c LOCUS DEFINITION
Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Pax: 81-59-81-6856 Email: tshinl@genes.nig.ac.jp The information of this clone is available through the following URL. http://xenopus.nibb.ac.jp.	Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus, Xenopus. 1 (bases 1 to 616) Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.	Laevis cuma Cione X1090]06 5', mRNA sequence. BJ074127.1 GI:17504316 EST. Xenopus laevis (African clawed frog) Xenopus laevis	BJ074127 616 bp mRNA linear BST 29-SEP-2003 BJ074127 NIBB Mochil normalized Xenopus tailbud library Xenopus

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RESULT 2
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Best Local Similarity:
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PRI0142b_B11 - PRIO142b_var. (
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survey sequence. CL662734
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                                                                                                              ArgAlaThrProLeu 293
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/mol_type="mRNA"
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/clone="XL090j06"
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dev stage="stage 25"
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library"
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1044.00
99.5%
99.5%
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                    953 bp DNA linear GSS 09-JUL-2004 PRI0142b.B21 (853) Mixed stage fosmid library of P. California Pristionchus pacificus genomic, genomic
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  GlnThrLeuGlnGlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGlu
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US-10-601-319-2 (1-440) x CL662734 (1-853)
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AppaDB: an AcedB database
Pristionchus pacificus
Nucleic Acids Res. 32 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: T7
Class: fosmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pax: 00497071601498
Email: rall:sommer@tuebingen.mpg.de
This library was generated at Caltech,
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyArgIleThrAspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPhe
                                                      PheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPhe 376
                                                                                                                   GAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTG
                                                                                                                                          GluLeuAsnTrpThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuVal 356
                                                                                                                                                                                                                     ThrSerValLeuPheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeu 336
                                                                                                                                                                                                                                                                              ATCATGGCAGCGTTGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCC
                                                                                                                                                                                                                                                                                                     IleMetAlaAlaLeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pristionchus p
/mol type="genomic DNA"
/strain="California"
/db xrefe="caxon:54126"
/clone lib="Mixed stage f
var California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector:
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Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G. Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU713770 529 bp mRNA linear EST 23-OCT-2003
SJAABUGG2 Adult SjC 7/94 Schietosoma japonicum cDNA similar to
pdb|IDKP|A Chain A, Crystal Structure Of Phytate Complex Of
Escherichia Coli Phytase At Ph 6.6. Phytate Is Bound With Its
3-Phosphate In The Active Site. Hg2+ Cation Acts As An
Intermolecular Bridge, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Zeguang Han
Chinese National Human Genome Cent
351 Guo Shoujing Road, Zhangjiang
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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Schistosoma japonicum
Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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EST.
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/lab host="Mouse and rabbit"
/clone_lib="Adult sjc 7/94"
/clone_lib="Adult sjc 7/94"
/clone_lib="Adult sjc 7/94"
/note="Vector: Lambda ZaP-II XR.; Site_l: EcoR I; Site_2:
/khol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oligo dT
chromatography, using a kit from Pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oligo-dT-XhoI-primer and synthesis was
primed with Roman library. First strand synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Whole body"
/dev_stage="Adult worms"
/lab_host="Mouse and rabb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Schistosoma japonicum"
/mol_type="mRNA"
/strain="Chinese (Anhui) strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Male and female"
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Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

RESULT 4 CA093060 SOURCE ORGANISM VERSION KEYWORDS REFERENCE DEFINITION US-10-601-319-2 (1-440) x BU713770 (1-529) ORIGIN ACCESSION Best Local Percent Similarity: Alignment Pred. No.: AUTHORS TITLE JOURNAL 364 481 421 344 301 324 241 304 181 284 121 264 244 LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 224 AlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe 243 61 Similarity: Vettore, A.L., da Silva, F.R., K The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-Saccharum officinarum Saccharum officinarum Saccharum officinarum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poalea; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum 9746 bp mRNA linear E SCCCCL2001D10.b CL2 Saccharum officinarum cDNA clone 3/, mRNA sequence. CA093060.1 GI:34946367 CA093060 GATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTG AspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeu SerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArg GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu GlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuPro GluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAlaLeuThrPro AGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGT GGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTA GGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGGACGCTTCCC CATCCACCGCAAAAACAGGCGTATGGTGACATTACCCACTTCAGTGCTGTTTATCGCC HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla GAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrPro GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT (bases 1 to 746) 1.08e-82 913.00 98.9% 98.9% 39.7% Length: Matches: Conservative: Mismatches: Indels: Kemper, B.L. and Arruda, P Saccharum; Saccharum officinarum 174 0 2 0 EST 23-SEP-2003 ne SCCCCL2001D10 528 263 480 383 420 360 343 300 323 240 303 283 120 60

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Email: parruda@unicamp.br
Clome distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 001 row: D column: 10
Seq primer: M13/Forward primer.
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                                                                                                                                          HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla
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GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu 363
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/lab_host="XL1Blue MRF'"
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/db_xref="taxon:4547"
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., L. Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clac; Ehrhartoideae; Oryzeae; Oryza.
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JMT1--05-B09.gl AtJMT-overexpressing transgenic rice lambda pha-
cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
clone JMT1--05-B09, mRNA sequence.
CP326092 CP326092
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
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                                                                                         SerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrProGluValAlaArgSerArg
GCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAG
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/dev stage="14 days after germination"
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end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
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Location/Qualifiers
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/mol_type="mRNA"
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                                                                                                                                                                                        UMR Bi03P, BP 35327, F-35653 Le Rheu Cedex France Tel: +33.2.33.48.51.65
Fax: +33.2.33.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphil Genomics in collaboration with Genoscope FORWARD: CAGGAAACAGCTATGACC Plate: 5 row: C Column: 9.
                                                                                                                                                                                                                                                                                                                                    Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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1 (bases 1 to 895)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
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CN762997
CN762997.1 GI:47536920
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/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic female
/lab_host="XL1-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: X
Sample name: IDDAAA; Plant growth place: Department
                                                                                       /organism="Acyrthosiphon pisum"
|mol type="mRNA"
|cultivar="developmentstage"
|db xref="taxon:7029"
|clone="IDOAAA5DC09"
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Location/Qualifiers
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Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/66/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
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SOURCE
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Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Rikaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Merazoa; Hemiptera; Sternorrhyncha; Aphidiformes;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 868)
Hunter,W., Martinez-Torres,D., Rahbe,Y., Sabater-Munoz,B.,
Stern,D., Tagu,D. and Wincker,P.
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.65
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
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Contact: D. Tagu
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/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: IDDAAA; Plant growth place: Department of
Bcology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction: ; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c) "
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/tlssue type="whole insect"
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                                                                                 US-10-601-319-2 (1-440) x CN757565 (1-864)
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Baraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 864)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
CN757565
CN757565.1 GI:47531488
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMR B103P, BP 35327, F-35653 Le
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2004)
Contact: D. Tagu
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1D0AAAA1DF09RM1 ApMS Acyrthosiphon
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                      ThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAlaLeu
ACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTG-ATCAAGACAGCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA 448
                                                                                                                                                                                                                                                                                                             /note=Tvector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: IDDAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Acyrthosiphon pisum"

/mol type="mRNA"

/cultivar="developmentstage"

/db xref="taxon:7029"

/clone="IDOAAA1DF09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
/clone_lib="ApMS"
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                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
I (bases 1 to 383)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B.,
Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C.,
Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato seed tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW036132
383 bp mRNA linear EST 18-MAY-2001 EST274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEELE23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036132
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                                                                                                                                                                                                                                                                                                                      Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                              Clemson University
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/mol type="mrNA"
/mol type="mrNA"
/cullivar="TA496"
/cullivar="TA496"
/db_xref="taxon:4081"
/clone="clebib23"
/tissue_type="seeds"
/dev_stage="quiescent seed"
/lab_host="Xi1-Blue MRF'"
/clone lib="tomato seed, TAMU"
/clone lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site 2:
Xho1; CLEE - Tomato Seed EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B.,
Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C.,
Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato seed tissue
                                                                                                                                   100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html 5 prime sequence.
                                                                                                                                                                                    Clemson University Genomics Institute Clemson University
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383 bp mRNA linear EST 18-MAY-200 ESTZ174510 tomato seed, TAMU Lycopersicon esculentum cDNA clone CLEELE23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036134

AW036134.1 GI:S894813
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                   /db_xref="taxon:4081"
/clone="clee1E23"
/tissue_type="seeds"
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                     M11B12STM Arabidopsis developing seed Arabidopsis thaliana clone M11B12 5', mRNA sequence.
                                                  Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                            1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                224 Biochemistry, Michigan State University,
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/lab host="XL1-Blue MRF" |
/clone_lib="tomato seed, TAMU"
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Xho1; CLEE - Tomato Seed EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site."
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Schistosoma japonicum
Schistosoma japonicum
Schistosoma japonicum
Eukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schist
                                                                                                                                 BU713769 531 bp mRNA linear EST 23-OCT-2003 SJAABUG01 Adult SjC 7/94 Schistosoma japonicum cDNA similar to sp|P07102|PPA_ECOLI PERIPLASMIC APPA PROTEIN PRECURSOR (INCLUDES: PHOSPHOANHYDRIDE PHOSPHOHYDROLASE (PH 2.5 ACID PHOSPHATASE) (AP);
                                                                   BU713769.1
EST.
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                                                                                                                   6-PHYTASE ], mRNA sequence.
                                                                                                                                                                                                                                                      ValSerLeuThrGlyAlaValSerLeuAlaSer 237
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                      244 LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 263
                                                                                                                                  224 AlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe
51
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Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chinese National Human
351 Guo Shoujing Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Zeguang Han
                                                                                                   GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /ucv_bruge="Adult Worms"

/(lab host="Mouse and rabbit"

/(clone lib="Adult $jC 7/94"

/note="vector: Lambda ZaP-II XR.; Site_1: EcoR I; Site_2: Xhol I; Several hundred adult Schistosoma japonicum (Anhui, P.R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRNA was isolated at the QIMR from lysates of these worms by oligo dT chromatography, using a kit from Pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dT-XhoI-primer and synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to EcoRI linkers, digested with EcoRI and XhoI, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QIMR. During analysis of the library at the QIMR, we have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Schistosoma japonicum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Whole body"
/dev_stage="Adult worms"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Male and female"
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                                                                                                                                                                                                                                                                     8.65e-50
591.50
79.5%
75.6%
25.7%
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Zhangjiang Hi-Tech Park, Pudong,
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Matches:
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133
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JOURNAL COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                   UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Teax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: D. Tagu
INRA Rennes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (Dases 1 to 706)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN759004 706 bp mRNA linear EST 20-MAY-20
IDOAAAA4BC04RM1 ApMS Acyrthosiphon pisum cDNA clone IDOAAA24BC04
5', mENA sequence.
CN759004
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Acyrthosiphon pisum
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                                                                                                                                                                                                                                                                                                                   PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAspLysThrProLeuSerLeuAsnThrProProGlyGlu 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 row: C
/clone_llb="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: IDOAAA; Plant growth place: Department of
                                                                 /clone="ID0AAA24BC04"
/tissue_tpe="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                                                   /mol_type="mRNA"
/cultivar="developmentstage"
                                                                                                                                                                                                               organism="Acyrthosiphon pisum"
                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                    db_xref="taxon:7029"
                                                                                                                                                                                                                                                                              column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the pea aphid Acyrthosiphon
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TITLE
JOURNAL
COMMENT
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AA545747/c
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VERSION
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                     Hominidae; Homo.

1 (bases 1 to 354)

Jia,L., Robey,P., Young,M., Schuler,G., Powell,J., Yang,L.,

Lennon,G., Hillier,L., Allen,M., Bowles,L., Geisel,S., Kucaba,T.,

Marra,M., Martin,J., Steptoe,M., Tan,F., Theising,B., Bowers,Y.,

Wylie,T., Waterston,R., Wilson,R. and Francomano,C.

WashU-MGB/NHGRI EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HBMSF1B4-REV Human Bone clone HBMSF1B4 5', mRNA
                                                                                                                                                National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda. Tel: 301-402-4877 Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                        Medical Genetics Branch
                                                                                                                                                                                                                                                               Contact: Libin Jia
                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA545747.1 GI:2307026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGluValLysLeuThrLeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSer 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValPheGlnThrLeuGlnGlnMetArgAspLysThrProLeuSerLeuAsnThrProPro 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACTGGAGCTCAACTGGACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAA
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                                                                                                        il: libin@helix.nih.gov
primer: M13 Reverse.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.73e-42
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Matches:
Conservative:
Mismatches:
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RESULT 15
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DB:
FEATURES
                                                                                                                                                                 COMMENT
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Best Local Similarity:
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                                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog)
Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 707)
                                                                             Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Cel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                   TSE
                                                                                                                                                                                                                                                                                                                                                                                                 BJ619443 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL189d24 5', mRNA sequence.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                                                                                                                 Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                  BJ619443.1 GI:37258203
                                                                                                                                                                                                                   Kohara,Y
                                                                                                                                                                                                                              Kitayama, A., Terasaka, C., Mochii, M.,
                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="bone marrow"
/cell_type="stromal fibroblast"
/dev_stage="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="XL1-Blue"
/clone_lib="Human Bone Marrow Stromal Fibroblast"
/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI"
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Source 1 ORIGIN Alignment Scores: pered. No.: Score: Percent Similarity: Dest Local Similarity: Query Match: DB: US-10-601-319-2 (1-440 Qy 251 MetProd1 Qy 251 MetProd2 Qy 271 LeuHisAs Qy 271 LeuHisAs	e /organism="Xenopus laevis" /mol_type="mRNA" /db xref="taxon:8355" /clone="XL189d24" /tissue_type="whole embryo" /dev_stage="stage 10.5" /clone_lib="NIBB Mochii normalized Xenopus early gastrula library" Scores: 2.66e-34
Alignment Sco Pred. No.: Score: Percent Simil Best Local Si Query Match: DB:	2.66e-34 Length: 442.00 Matches: 97.6% Conservative: 19.2% Indels: 2 Gaps:
US-10-601-319	(1-440) x BJ619443
	MetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsnThrLeuLeuSer
	LeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrProGluValAlaArgSerArgAla
Db 62 Qy 291	TigeATAAcigeGeAATTTTATTTGETACAAcigeAcigeCAGAGGTTGCCCGCAGCGGCGCC 121 ThrProLeuLeuAspLeuIleMetAlaAlaLeuThrProHisProProGlnLysGlnAla 310
Db 122	ACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAAACAGGCG 181
Qy 311 Db 182	TYTGTYVATThrLeuProThrSerValLeuPheIleAlaGlyH18AspThrAsnLeuAla 330
Qy 331 Db 242	

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FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-12-11
PRIOR PILING DATE: 2002-12-11
NUMBER OP SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27838
LENGTH: 3731
TYPE: NNA
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ORGANISM: OTYZA BALLIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103280
DATABASE ENTRY DATE: 2002-08-28
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284 GluValAlaArgSerArgAlaThrProLeuLeuAsp-------LeuIle 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GluAlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThr-----
                                                                                                                          GlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsn
                                                                                                                                                              CAACTCTCCTCTCTCAGTCTTCACCTATGACACTGCAAACAGTATTACCATTCTCC
                                                                                                                                                                                                                               CAACAGCAGAAGAACATGACCAACTATCAGTCTGTACCTAATGCATTGTCACCGTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                              GlySerIleAlaAspPheThrGlyHisArgGlnThrAlaPhe-----ArgGluLeuGlu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCTTCCTTACTTGGTCTGCAACCTGACATGTATCAAACGATAGCTGCGACTGCTTTC 2058
                              ACA---TCCACCATGCATAATGCATTGAGGCCATTTTCATCGGAAGCACCTTCGCACCTA 2610
                                                             ThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGlnArgThrPro-----
                                                                                               CAGCCACAGAGCTATCCAGACACGAGTATGAGCTCATTATCACCATCC-----AAC
                                                                                                                                                                                               TCACAGCAACAACAGCAGCAGCAATCGCAGTGTATGCAAGTCCCACAACATCAGCAAATG
                                                                                                                                                                                                                                                                                                                               CysSerLeuThrGlnAlaLeuProSerGluLeu--------
                                                                                                                                                                                                                                                                                                                                                          CGCTGCCAGTCGTTTACTGAGCAGAAGCCACAGCTGCAAACCCCAGCAACAACAGCAAGAA 2322
                                                                                                                                                                                                                                                                                                                                                                                          ArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGluSer 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCAGCAGCAATACCTCCAAAACATCAACGAGACC-----
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                                                            428
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                                                                                                                                                                                                                                                 CCGTCGCAGAATGATTTCCCCCTTGGATCAAACACTAAGTAGTGCAGACTGCTTAGATGAA 300
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                                                                                                                                                                                                                                                                                                                                                                                   AGCCTCCAGGGTGAGAATGATTCGACGGCAATTCCTTATTCCACCTCCAATTTCCTGAGC 2943
CCTGCG
                                                            ProAla 429
                                                                                                                        TCAGGATATGTGCCGTGTTCA---CAGAATTCTGATCAAGTGATTAAT-----CGACCA 3054
                                                                                                                                                                                 AsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGlnIleValAsnGluAlaArgIle 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ### TIGGAGTCTTTGCTTCCTCGTCCTCAGGTTACATCGCAGATGGAGCAGTTGGACTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGln 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AGAGGATGCTTGGTGGATCAAGATGGGAACTCTGATCCTCAAAAACCATCTGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAsnTrpThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPhe 357
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3060
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	; APPLICANT: The Institute of Physical and Chemical Research. ; APPLICANT: Foundation for Advancement of International Science. ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
1864 GCTGAACAAGAACTGGGGGATTGAGGTCAGACCCC	Db 327 GGCGATGGATTACTGGCTCGTTCTCCGGGGGCGCCGGGGACATCTTCGACGCCAT 386 Qy 96LysLysGlyCysProGlnSerGlyGlnVal

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Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 34901, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REPRENENCE: 2750-1579PUS2
CURRENT PAPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SOFTWARE: PatentIn version 3.3
LENGTH: 1619
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US-10-953-349-34901
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                                                     350 oproGlyGlyGluLeuValPheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIl
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Publication No. US20060111297A1
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce
TITLE OF INVENTION: BLOOD FACTOR DOMAINS
FILE REFERENCE: 5270C
CURRENT APPLICATION NUMBER: US/11/297,134
CURRENT APPLICATION NUMBER: US/11/297,134
PRIOR FILING DATE: 2005-12-08
PRIOR APPLICATION NUMBER: PCT/US2005/018461
PRIOR FILING DATE: 2004-06-09
PRIOR PILING DATE: 2003-06-09
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Parentin version 3.3
SEQ ID NO 55
LENGTH 1502
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US-11-297-134-55
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                                  TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-505-928-570
SEQ ID NO 570
LENGTH: 14756
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; Publication No. US20060088532A1
; GENERAL INFORMATION:
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITILE OF INVENTION: FULL-LENGING CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT PILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-29
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12801
LENGTH: 3287
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK110149
DATABASE ENTRY DATE: 2001-12-06
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                                                                                                                                         AA----GAAAAGAGCCGCAACATGGAGGAGCGGCTCAAAGATACCGAGGGCATCATG-
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FULR REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR PILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PATENTIN 3.2
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1597 CCTCCCAAG-----ACGCCCACCATGACTGTTTTTGTGGAGCCC 4635
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                                                                                                                                                                                                              204 GluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSer 223
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  lyHisArgGlnThrAlaPheArgGluLeu
                                                    *168 CATGGGGTCCACGGCTTAGCAGTGGGGACAGGCCATGTCCAGGTGGCCCGCAACGCCCTG
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                                                                                                       Glu---ArgvalleuAsnPheProGlnSerAsn----
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Publication No. US20060105376A1
GENERAL INPOWATON:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
FRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
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1183 AAATCACCTAAAGGCTCTTTCAAAATAAGGATGTGTTACTCTCCAAAGAC-----
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1957
LENGTH: 1945
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Best Local Similarity:
                                                        ; TYPE: DNA
; ORGANISM: Homo
US-11-293-697-1957
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ORGANISM: Sus scrofa
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Best Local Similarity:
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               119 AAG------GTGGTGGAGAAGATTGGGGACTACAAACGCCAGAACCCTACCATGTTT 469
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                                                                      199 ATCTCTCGCCAGCTCCGCGTCAGCCATGGCTCAGCAAGATCCTTGGCAGGTACTAC 358
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                                               ArgGlyGlyGluLeuIleAlaTyrLeuGlyHisTyrGlnArgGlnArg------
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329 ualaasnieuGlyGlyalaLeuGluLeuAsnTrpThrLeuProGlyGlnProAspAsnTh 349
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1991 GTIGCCCTICTIGCCGAGGCTGACGGIGTACTCGAGGCGGAGCTGCTTGAGCTCCTC 1932
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Sequence 189, Application US/11145307A

Publication No. US20060094035A1

GENERAL INFORMATION:
APPLICANT: Arcturus Bioscience, Inc.
APPLICANT: Rilander, Mark G.
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Identification of Tumors
FILE REFERENCE: 022041-002020US
CURRENT PILING DATE: 2005-06-03

PRIOR APPLICATION NUMBER: US 60/577,084
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SOFTWARE: Patentin version 3.1
SEQ ID NO 189
LENGTH: 2711
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CRGANISM: Homo sapiens
US-11-145-307A-189
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                                            244 CTIGGCCGCCACCACCACCTTCATCGCCTCCGTGATCTTCTGCGTGTTGCGCAC-CGAGT 186
                                                                                                                                                                                         nValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeuGl 246
                 uleuGluArgValLeuAsnPheProGlnSerAsnLeu---CysLeuLysArgGluLysGl 206
                                                                                                    nAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspAs 226
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT CONA AND USES THEREOF
FILE REPERBRÜCE: MOA-AO205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR PILING DATE: 2003-05-29
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SEQ ID NO 7723
LENGTH: 2822
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; PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: AK105071

; DATABASE ENTRY DATE: 2002-08-28

US-10-449-902-7723
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US-10-449-902-21879/c
US-gequence 21879, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement In
APPLICANT: The Institute of Physical and Chemical Research
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TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT PILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21879
LENGTH: 1470
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072104
DATABASE ENTRY DATE: 2001-12-06
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                                                                                                                                                                              SerSerProAsp-----ProLeuPheAsnProLeuLysThrGly-----
                                                                                                                                                                                                               GATGCGGGTCTCGGCCTTCTTGAGGACGTTGTTGTTGAAGCTGCCGCAGAGGCCGCGCTC
                                                                                                                                                                                                                                                  AlaAlaGlyLeuAla----ProAspCysAlaIleThrValHisThrGlnAlaAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                              CTCGGACACGAACAGCGAGTAGACGAGGTCGCAGATGGACTGGGAGTCCTTCACGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuGlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGCGGACGAGGGAGACGAACTTGG-----AGTAGAGGAGCTCCACCTTGTCCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGCAGATCTCCCCCT----TGGGCGACATGGGGAGCAGCGTCTGGATGATGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tGlnAspValThr-ProAspAlaTrpProThrTrpProValLysLeuGly-----
                                                                                                                                                                                                                                                                                                                                                                                        -----CysproGlnSerGlyGln-----
                                    -----AlaGlyGlySerIleAlaAspPheThrGlyHisArg-GlnThrAlaPheArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GluLeuIleAlaTyr 79
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5.0%
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Length: Matches: Conservative: Mismatches: Indels:

1470 83 30 108 82

(1-1470)

104 587 98 647 67 755 51 791

-GluAlaPhe

467 122

287 187

169

407

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Result
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-Q=/abss/ABSSWEB_spool/US10601319/runat_12062006_180105_27789/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10601319/runat_12062006_180105_27789/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUPFIX=rnpbn -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -HOST=abss03h
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                               118
114.5
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113.5
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101.5
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           86
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
                                                                                                                                                                                                                       Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA_New:*

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2. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*

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8. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US00_NEW_PUB.seq:*
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Ygapext
Fgapext
Delext
  US-10-449-902-14217

US-10-449-902-21879

US-10-449-902-7723

US-11-145-307A-189

US-11-270-040-5

US-11-293-657-1957

US-11-217-529-274

US-10-505-928-570
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4595.351 Million cell updates/sec
Sequence 21879, A
Sequence 7723, App
Sequence 189, App
Sequence 5, Appli
Sequence 1957, Ap
Sequence 274, App
Sequence 12801, A
Sequence 570, App
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Sequence 21879, A
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US-10-449-902-11507	-10-449-902-	-11-293-697-	-11-293-697-5	-10-449-902-114	-11-217-529-	-10-489-730-	-11-118-524-	-10-449-902-1	1-293-697-3	-11-293-697-1200	-10-449-902-2666	-10-449-902-134	-10-449-902-2201	-10-449-902-149	93-697-1	-11-293-697-9	-10-449-902-161	-10-953-349-8	-10-511-937-358	-11-293-697-1	-10-449-902-201	-10-528-659-	-09-949-925-	-11-284-978-1	501-834-	-10-511-937-5	-11-293-697-8	-10-449-902-126	S-11-293-697 -14 8	S-10-449-902-2783	S-10-449-902-2458	S-10-449-902-2	-10-449-902-2011	-10-953-349-3	1-297-134-5
e 115	e 222	equence 815,	equence 518, F	equence 1140	e 2750,	INFORM	e 1, A	12653	Sequence 315, App	e 1200,	e 26664,	e 13489,	Sequence 22017, A	e 1494,	e 1467,	946,	Sequence 16137, A	Sequence 8294, Ap	358,	Sequence 1085, Ap	20	6	Sequence 71, Appl	14	1	54	equence 84	equence 12	equence 1489,	equence 27838	equence 24588,	equence 26929,	equence 20112,	equence 34901,	S .

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a

a

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a

RESULT 1

US-10-449-902-14217/c

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Percent Similarity:
Best Local Similarity:
                                               Score:
                                                                          Alignment Scores: Pred. No.:
                                                                                                                                           ; PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK064835;
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-14217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14217, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14217
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REPERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR PILING DATE: 2002-05-30
PRIOR PILING DATE: 2002-12-11
NUMBER: OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                           LENGTH: 1482
0.0336
118.00
34.9%
24.8%
                      Length:
Matches:
Conservative:
Mismatches:
74
30
116
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Appli Appli Appli Appli

us-10-601-319-2.rnpbm

Scoring table:

Total number

Searched:

Perfect score:

Sequence:

OM protein

Run on:

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Sequence 3, Appli
Sequence 9, Appli
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Sequence 5, Appli
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Sequence 7, Appli
Sequence 5, Appli
Sequence 9338, Ap
                                                                               Sequence 1, Appli
Sequence 7167, Ap
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 3181, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24247, A
Sequence 30120, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Sequen
   Sequence 1, A
Sequence 1, A
Sequence 1, A
Sequence 1, A
3 US-09-866-379-1

6 US-10-034-985-1

7 US-10-034-985-1

8 US-10-601-319-1

9 US-10-282-128-7167

3 US-10-282-128-7167

6 US-10-661-319-7

10 US-10-933-115-7

14 US-11-056-354-3

10 US-10-933-115-7

14 US-11-061-319-6

10 US-10-933-115-6

10 US-10-933-115-6

11 US-10-601-319-6

12 US-10-866-379-6

13 US-08-866-379-6

14 US-10-01-319-9

15 US-10-01-319-9

16 US-10-933-115-6

17 US-10-933-115-6

18 US-10-01-319-9

19 US-10-933-115-9

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11 US-11-018-709-4

6 US-10-933-115-9

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11 US-11-018-709-4

6 US-10-933-115-9

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10 US-10-933-115-9

10 US-10-334-672-4

11 US-10-334-672-4

12 US-10-282-122A-41608

6 US-10-021-723A-9

10 US-10-282-122A-3181

10 US-10-282-122A-3181

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1126.5
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                                                                                                                                                    (without alignments)
5637.400 Million cell updates/sec
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                                                                                                                                                                                                        US-10-601-319-2
2302
1 MKAILIPPLSLLIPLTPQSA.....IVNEARIPACSLRSHHHHHH 440
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                                                                                                                              June 14, 2006, 14:19:34 ; Search time 1438.58 Seconds
                   GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                           - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                    18892170 seqs, 6143817638 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length DB
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Score

Result

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                                                                                                  LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320
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     781 GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09866379

Sequence 1, Application US/09866379

Patent No. US20020136754A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: REXTZ, Kevin

APPLICANT: GRARIT, Jane

APPLICANT: GRARET, Jane

APPLICANT: OFFICE OFFICE

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2001-05-24

PRIOR FILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1997-08-13

PRIOR FILING DATE: 1997-08-13
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                                                                                                                                                                                                                                                                                               ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KRY: misc feature
LOCATION: (1). (1323)
OTHER INFORMATION: n is any nucleotide
NAME/KRY: CDS
LOCATION: (1). (1323)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Escherichia coli
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) ORGANISM: Escherichia coli

) FEATURE:

) NAME/KEY: CDS

) LOCATION: (1)..(1320)

) NAME/KEY: misc_feature

) LOCATION: (1)...(1323)

) OTHER INFORMATION: n is any nucleotide

US-09-777-566A-1
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                                                                                                                                                                                                                                                                     Sequence 1, Application US/10034985
Publication No. US20030049815A1
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
ITILE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/580,515
FRIOR APPLICATION NUMBER: US/09/580,515
FRIOR APPLICATION NUMBER: US/09/580,515
FRIOR APPLICATION NUMBER: US/09/590,515
FRIOR APPLICATION NUMBER: 09/291,931
FRIOR APPLICATION NUMBER: 08/910,798
FRIOR APPLICATION NUMBER: 08/910,798
FRIOR APPLICATION NUMBER: 08/910,798
FRIOR FILING DATE: 1999-03-01
NUMBER: OSEQ ID NOS: 4
SOUTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
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ORGANISM: Becherichia coli
FEATURE:
NAME/KEY: CDS

LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)

OTHER INFORMATION: n = A,T,C ox
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TYPE: DNA

ORGANISM: Escherichia coli
FRATURE:
NAME/KEY: CDS

FRATURE:
NAME/KEY: misc_feature

LOCATION: (1)...(1320)

FRATURE:
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COTHER INFORMATION: n = A,T

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Percent Similarity:
Best Local Similarity:
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                 LeulysargglulysglnaspgluserCysSerLeuThrGlnalaLeuProSerGluLeu
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                                                GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCAGGAGATACG
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Publication No. US20040091968A1

GENERAL INNORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Short, Jay M.
APPLICANT: Gray, Kevin A.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Elleen
FRIGR REFERENCE: 0901-02901
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: 1099-03-01
PRIOR PLING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/214
PRIOR APPLICATION NUMBER: US 09/214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOGTHWARE: PERSEEQ for Windows Version 4.0 1323 440 0 0 0 Length:
Matches:
Conservative:
Mismatches: US-10-601-319-2 (1-440) x US-10-601-319-1 (1-1323) NAME/KEY: CDS
LOCATION: (1)...(1320)
FEATURE:
FEATURE:
LOCATION: 216
OTHER INFORMATION: n = A,T,C or G Ö 1.32e-261 2302.00 100.0% 100.0% TYPE: DNA ORGANISM: Escherichia coli 음

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RESULT 5 US-10-601-319-1

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APPLICANT: Kretz, Keith A.
APPLICANT: Garat, Kevin A.
APPLICANT: Garaton, Nelson Robert
APPLICANT: Garrent, James B.
APPLICANT: Garrent, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Wathur, Bric J.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPRENCE: 56446201822
CURRENT APPLICATION NUMBER: US/09/866,379
PRIOR PLILNG DATE: 2001-05-24
PRIOR PLILNG DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR PLILNG DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PLILNG DATE: 1999-04-13
PRIOR PLILNG DATE: 1999-04-13
PRIOR PLILNG DATE: 1999-04-13
PRIOR FILING DATE: 1997-08-13
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FRATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
FRATURE:
NAME/KEY: misc_feature
LOCATION: 216
OTHER INFORMATION: n = A,T,C or
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Length:
Matches:
Conservative:
Mismatches:
Indels:

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Sequence 1, Application US/10933115; Publication No. US20550281792A1; GENERAL INFORMATION: APPLICANT: Short, Jay M.

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APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Yu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Sold of the Military of Military 
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Pred. No.:
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                                                                                                                                                                                                      LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
AACGTGACTGACGCGATCCTCAGCAGGCAGGAGGGTCAATTGCTGACTTACCGGGCAT
                                                                                                                                                                                                                                                          LeulysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
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Matches:
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                                                 1.12e-253
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; ORGANISM: Escherichia coli
US-10-282-122A-7167
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Percent Similarity:
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Query Match:
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; Sequence 7167, Application US/10282122A ; Publication No. US20040029129A1 ; GENERAL INFORMATION: ; APPLICANT: Wang, Liangsu ; APPLICANT: Ralone, Cheryl ; APPLICANT: Haselbeck, Robert ; APPLICANT: Haselbeck, Robert

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LOCATION: (1). (1901)
OTHER INFORMATION: n is any
                                                                                                                                                  TYPE: DNA ORGANISM: Escherichia coli
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Query Match:
DB:
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Sequence 7, Application US/09866379; Patent No. US20020136754A1; GENERAL INFORMATION:
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith

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APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRET, James
APPLICANT: GARRET, James
APPLICANT: GARRET, James
APPLICANT: O'DONGGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERLAJ70-7
CURRENT APPLICATION NUMBER: US 09/586,379
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 1000-05-25
PRIOR PLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR PLICATION NUMBER: US 09/291,931
PRIOR PLICATION NUMBER: US 08/210,798
PRIOR PLING DATE: 1999-03-01
PRIOR PLING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALEALIN VERSION 3.1
SEQ ID NO 7
LENGTH 1901
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181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200
 PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
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PRIOR PILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
SEQ ID NO 3
                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 403
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity:
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; Publication No. US20030103958A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Barton, Velen A.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Gartet, James B.
; APPLICANT: Gartet, James B.
; APPLICANT: HIVENTON: ENTRASE, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: PHYTASES, VIOLEIC ACIDS CONTROL OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REPERENCE: 09010-029007
; CURRENT APPLICATION NUMBER: US/10/156,660
; CURRENT FILING DAIR: 2002-10-01
; PRIOR APPLICATION NUMBER: US 09/866,379
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  PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION WUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR PLING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER: OF SEQ ID NOS: 10
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NAME/KEY: CDS
LOCATION: (188)...(1483)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 403
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                                                                                                         CTTAAACGTGAGAAACAGGACGAAGGTGTTCATTAACGCAGGCATTACCATCGGAACTC
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PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-13
SOSTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 7
TYPE: DNA
TYPE: DNA
NAME/KEY: CDS
NAME/KEY: CDS
LOCATION: (188)...(1483)
FRATURE:
NAME/KEY: Misc_feature
NAME/KEY: US
COCATION: 403
NAME/KEY: US
COCATION: 403
COTHER INFORMATION: n = A,T,C or G
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                                                     JULY SEQUENCE 7, Application US/1093315

Publication No US20050281792A1

FORDERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Gray, Kevin A.

APPLICANT: Garrett, James B.

APPLICANT: Mathur, Elic J.

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES

TITLE OF INVENTION: TRECOMBINANT BACTERIAL PHYTASES AND USES

FRIOR FILING DATE: 2001-05-03-04

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR PLILING DATE: 1999-04-131

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ORGANISM: Escherichia coli app

FRATURE:

NAME/KEY: misc feature

LOCATION: (403)...(403)

OTHER INFORMATION: n is any nu
US-11-056-354-3
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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Pred. No.:
                                                               LENGTH: 1901
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                                              GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArglleThr 260
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| CS-quence 3, Application US/11056354
| Publication No. US20050246780A1
| GENERAL INFORMATION:
| APPLICANT: SHORT, Jay M. |
| APPLICANT: GRAY, Kevin A. |
| APPLICANT: GRAY, Kevin A. |
| APPLICANT: GARRET, James B. |
| APPLICANT: GARRETY, Walson R. |
| APPLICANT: GARRETY James B. |
| APPLICANT: MATHOR, FIFTA JAMES B. |
| TITLE OF INVENTION: FOR MAXING AND USING THEM AND METHODS FILLS FOR INVENTION: FOR MAXING AND USING THEM CURRENT FILING DATE: 2005-02-11 |
| PRIOR APPLICATION NUMBER: US 09/586,379 |
| PRIOR FILING DATE: 2000-05-25 |
| PRIOR FILING DATE: 2000-05-25 |
| PRIOR FILING DATE: 1999-05-25 |
| PRIOR APPLICATION NUMBER: US 09/291,931 |
| PRIOR FILING DATE: 1999-04-13 |
| PRIOR FILING DATE: 1999-03-01 |
   LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
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AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280
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; NAME/KEY: misc_feature
; LOCATION: 403 _
; OTHER INFORMATION: n = A,T,C
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Percent Similarity:
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Best Local Similarity:
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Query Match:
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                    ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla
                                                                         PhellealaglyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
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APPLICANT: Short, Jay M.
APPLICANT: Ketz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Elleen
APPLICANT: O'Donoghue, Elleen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEM
TITLE OF INVENTION NUMBER: US 09/866,379
PRIOR PLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                ; Sequence 6, Application US/10601319; Publication No. US20040091968A1; GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: Escherichia coli
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US-10-601-319-6
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Best Local Similarity: 99.3% Mismatches: 3 Query Match: 96.7% Indels: 0 DB: 3 Gaps: 0	-10-601-319-2 (1-440) x US-09-866-379-9 (1-1901)	Qy 1 MetlyaAlalleLeulleProPheLeuSerLeuLeulleProLeuThrProGlnSerAla 20 	Qy 21 PheAlaGlnSerGluDroGluLeuLyBLeuGluSerValValIleValSerArgHisGly 40	Qy 41 ValargalaProThrLysalaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	Qy 61 ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80 	Qy 81 GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100	Qy 101 GlnSerGlyGlnValAlaileileAlaAspValAspGluArgThrArgLysThrGlyGlu 120	Qy 121 AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 141 SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160	Oy 161 ASDVAlThrASPAlaIleLeuSerArgAlaGIyGIySerIleAlaAspPheThrGIyHis 180	Oy 181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200	Oy 201 LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220	Oy 221 LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	Qy 241 GluilePheLeuLeuGlnGlnAlaGlnGlyMet ProGluProGlyTrpGlyArglleThr 260	Qy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280	Oy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla 300	301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 32	321 Phelleands yet was a second control of the cont
1028 CGCACGCCAGAGGTTGCCCGCAGCCGCCCCCCTTATTAGATTTGATCAAGACGG 10	OY 301 LeafinFyChisProChidly8GlmAlaTyrClyVarThrLeaFroffrSerValleu 320	Oy 321 PhellealaGlyHisAspThrAsnLeualaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	ThrieuProGlyGlnBroAspAsnThrProProGlyGlyGlyGluLeuValPheGluArgTrp	361 ArgArgLeuSerAspAsnSerGlnTrplleGlnValSerLeuValPheGlnThrLeuGln 38	381 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 40	401 LeualaglyCysGluGluArgAsnAlaglnGlyMetCysSerLeualaglyPheThrGln 42	421 IleValAsnGluAlaArgIleProAlaCysSerLeu 432	SULT 14 -09-866-379-9	, SE .	; APPLICANT: SHORT, Jay ; APPLICANT: KRETZ, Keith ; APPLICANT: GRAY, Kevin ; APPLICANT: GRAY, Nelson	; AFFLICANT: GARKETT, James ; APPLICANT: O'DONOGHUE, Elleen ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF ; FILE REFERENCE: DIVER1370-7	TION NUMBER: US NUMBER: US NUMBER: US TE: 2000-05-25)9/318,)9/291,		<pre>; NUMBER OF SEQ ID NOS: 10 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 9 ; LENGTH: 1901</pre>	; TYPE: DNA ; ORGANISM: Escherichia coli ; FEATURE: · NAME/KRY. misc feature	; LOCATION: (1): (1901) ; OTHER INFORMATION: n is any nucleotide US-09-866-379-9	Alignment Scores: 2.27e-252 Length: 1901 Pred. No.: 2226.00 Matches: 429 Percent Similarity: 99.3% Conservative: 0

101 GlnSerGlyGlnValAlaileileAbabyalAspGluArgThrArgLysThrGlyGlu	0y 201 LeuLysArgGluLysGluAspGluSarCysSerLeuThrGluAlaLeuProSerGluLeu 220 Db 782 CTTAACCGTGAGAAACAGGAAGCTGTT[321 PhellealadlyHisAspThrAsnLeualaasnLeudlydlyAlaLeudluLeuasnTrp 34 321 PhellealadlyHisAspThrAsnLeualaasnLeudlydlyAlaLeudluLeuasnTrp 34 322 THATTATTCCGGACACGATACTAGCAAATCTGGCAAATCTCGGCACTCGGCGCCACTCGGCTCCAACTGG 334 ThrLeuProGlydlhProAspAsnThrProProGlydlyGluLeuValPheGluArgTrp 36 325 AcGCTTCCAGGCCGGATAACACGCCGCCCAGGTGGTGATTTGAACGCTGG 12 326 AcGCTTCCAGGTCAGCCGGATAACACGCCGCCAGGTGGTGATTTGAACGCTGG 12 337 ArgargLeuSerAspAsnSerGlnTrplleGlnValSerLeuValPheGlnThrLeuGln 38 338 ArgargLeuSerAspAsnSerGlnTrplleGlnValSerLeuValPheGlnThrLeuGln 38 339 GlnMetArgAspLygThrProLeuSerLeuAsnThrProProGlyGluValLygLeuThr 40 339 GlnMetArgAspLygThrProLeuSerLeuAsnThrProProGlyGluValLygLeuThr 40 330 GlnMetArgAspLygThrProLeuSerLeuAsnThrProProGlyGluValLygLeuThr 40 331 GlnMetArgAspLygThrProLeuSerLeuAsnThrProProGlyGluValLygLeuThr 40 332 CAGATGCGTGATAAAACGCCGCTATCATTAAATACGCCGCCGGGGGGGG	
8 8 <td>6</td> <td>: 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6</td> <td></td>	6	: 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6	
Qy 341 ThrLeuProGlyGlnBroAspAsnThrProProGlyGlyGlyLeuValPheGluArgTrp 360 Db 1208 ACGCTTCCCGGTCAGCCGGCCAGGTGGTGTTTGAACGCTGG 1267 Qy 361 ArgArgLeuSerAspAsnSerGlnTrp1leGlnValSerLeuValPheGlnThrLeuGln 380 Db 1268 CGTCGGCTAAGCGGTAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG 1327 Qy 381 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400 Db 1328 CGACGGTGATAAAATACGCCGCCGCGGAGAGGTGAACTGACC 1387 Qy 401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420 Db 1388 CTGGCAGGATGTGAAAAGCCCAGGGCATGTCTTCGTTGGCAGGTTTACGCAA 1447 Qy 421 IleValAsnGluAlaArglleProAlaCysSerLeu 432 Pb 1448 ATCGTGAATGAAGCCATACCGGCGTGAGTTTG 1483	RESULT 15 US-10-266-041-9 i Sequence 9, Application US/10266041 j Publication No. USZ0030072844A1 j GENERAL INFORMATION: APPLICANT: Lei, Kingen TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY FILE REFERENCE: 19603-7791 CURRENT FILING DATE: 2002-10-07 PRIOR APPLICATION NUMBER: US/10/266,041 PRIOR APPLICATION NUMBER: US/09/540,149 PRIOR PLING DATE: 1999-03-31 PRIOR PLING DATE: 1999-03-31 PRIOR PLING DATE: 2000-03-31 PRIOR PLING DATE: 2000-03-31 PRIOR PLING DATE: 1999-03-31 SOFTWARE: PATENTIN VOY: 2.1 SEQ ID NOS: 9 LENGTH: 1489 TYPE: DNA ORGANISM: Escherichia coli US-10-266-041-9	Alignment Scores:	422 GGACATTACCAACGCCAGCGTCTGGTGGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCG

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Perfect score:

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Sequence 23, Appl
Sequence 32, Appl
Sequence 32, Appl
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US-09-115-477-2
US-09-715-477-4
US-09-715-477-4
US-09-715-477-4
US-09-489-039A-5330
US-08-920-827-23
US-08-920-828-11
US-09-63-504-32
US-09-63-504-32
US-09-63-504-32
US-09-949-016-3481
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Sequence 1, Application US/09259214A

Patent No. 6110719

GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVER1370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT APPLICATION NUMBER: 08/910,796
BARLIER RILING DATE: 1999-03-01

BARLIER PILING DATE: 1999-03-01

SARLIER PILING DATE: 1999-03-01

SARLIER PILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1323
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| NAME/KEY: misc feature
| LOCATION: (1)...(1323)
| OTHER INFORMATION: n = A,T,C or US-09-259-214-1
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Percent Similarity:
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     Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q={Abs8/ABS/WEB spool/VB10601319/runat_12062006_180055_27578/app_query.fasta_1
-Q={Abs8/ABS/WEB spool/VB10601319/runat_12062006_180055_27578/app_query.fasta_1
-DB=ISBUSGA_PATE-BESTATE-ISTA_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_STATE_S
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2. /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3. /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
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5. /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
6. /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*
7. /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8. /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
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Sequence 1, 3
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                      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-318-528-1
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                                   361 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                Sequence 1, Application US/09318528
Fatent No. 6183740
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT FILING DATE: 1999-05-25
CURRENT APPLICATION NUMBER: 08/291,931
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER PILING DATE: 1999-04-13
EARLIER FILING DATE: 1997-08-13
EARLIER PILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/291,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Escherichia coli
FRATURE:
NAME/KEY: CDS
LOCATION: (1) ... (1320)
NAME/KEY: misc_feature
LOCATION: (1) ... (1323)
OTHER INFORMATION: n = A,T,C or G
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Fatent No. 6190897
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION:
FILE REFERENCE: 09010/02903
CURRENT PILLING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER PILING DATE: 1999-03-01
EARLIER PILING DATE: 1999-03-01
SEQIER FILING DATE: 1999-03-01
SOFTWARE: FASTSEQ for Windows Version 4.0
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LENGTH: 1323 Ö ö 1.05e-233 2302.00 100.0% 100.0% 100.0% A, I, C | FEATURE: | NAME/KEY: CDS | LOCATION: (1)...(1320) | NAME/KEY: misc_feature | LOCATION: (1)...(1323) | OTHER INFORMATION: n = A US-09-291-931-1 TYPE: DNA ORGANISM: Escherichia Percent Similarity: Best Local Similarity:

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SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
TITLE OF INVENTION:
GURRENT APPLICATION NUMBER: US/05/80,515
CURRENT APPLICATION NUMBER: 09/318,528
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-06-25
PRIOR PRILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1997-08-13
PRIOR PILING DATE: 1997-03-01
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: n is
; NAME/KRY: CDS
; LOCATION: (1)..(1323)
; OTHER INFORMATION:
US-09-866-379-1
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Query Match:
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GAGATATTTCTCCTGCAACAAGACACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 780
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Sequence 1, Application US/09866379

PRECENT NO. 6855365

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: RETZ, Keith

APPLICANT: GRRETZ, Keith

APPLICANT: GRRETT, Jahen

APPLICANT: GRRETT, Jahen

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

TITLE OF INVENTION NUMBER: US 09/586,379

CURRENT FILING DATE: 2001-05-24

PRIOR FILING DATE: 1999-04-13

PRIOR PLICATION NUMBER: US 09/291,931

PRIOR PLING DATE: 1999-04-13

PRIOR PLING DATE: 1999-04-13

PRIOR PLING DATE: 1999-03-01

SOFTWARRE PLING DATE: 1
                            CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
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Mismatches:
Indels:
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nucleotide
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### Execut Similarity: 99.54 ### ###############################	1028	Oy 321 PhelleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340
841 CGCACGCCAGAGGTTGCCCCCAGCCGCGCCCCCCTTATTGATTTTATCATGGCCGCGGGGGGGG	NAME/KEY: misc_feature LOCATION: (1)[1901) COTHER INFORMATION: n is any nucleotide US-09-866-379-7	Alignment Scores: 2.34e-226 Length: 1901 Pred. No.: 2235.00 Matches: 430 Score: Similarity: 99.5% Conservative: 0

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                                                                                                                                                      GlyHisTyrGlnArgGnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro
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Sequence 9, Application US/09866379

Patent No. 685365

GENERAL INFORMATION:

APPLICANT: BIOTORS CORPORATION

APPLICANT: SHORY, Jay

APPLICANT: SHORY, Jay

APPLICANT: BARTON, Nelson

APPLICANT: O'DONOGHUB, Elleen

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

FILE REPERRNES: DIVERAIN 07

CURRENT FILING DATE: 105/09/866,379

CURRENT FILING DATE: 2000-05-24

PRIOR FILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-03-01

PRIOR PILING DATE: 1999-03-01
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; OTHER INFORMATION: n is any nucleotide US-09-866-379-9
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99.3%
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Best Local Similarity:
Query Match:
DB:
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                                                                       CTTAACCGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATTGGAACTC
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   AsnvalThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                     LeuLysargGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
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; Sequence 9, Application US/10266041A
; Patent No. 6974690
; GRNERAL INFORMATION:
; APPLICANT: Lei, Xingen
; TITLE OF INVENTION:
; FILE REPERENCE: 19603/2798
; CURRENT APPLICATION NUMBER: US/10/266,041A
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/127,032
; PRIOR PLING DATE: 1999-03-31
; PRIOR FILING DATE: 2000-03-31
; RIOR FILING DATE: 2000-03-31
; NUMBER: OF EQUENCE OF EXAMPLE OF EXAMPL
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LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
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                                                                                                                                                                                                                                    ; Sequence 9, Application US/09540149A
; Parent No. 6511699
; GENERAL INFORMATION:
    APPLICANT: Led, Xingen
    TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
    FILE REFERENCE: 19603/2791
; CURRENT APPLICATION NUMBER: US/09/540,149A
; CURRENT PILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/127,032
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 9
; SEQ ID NO 9
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Matches:
Conservative:
Mismatches:
Indels:
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2221.00
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Best Local Similarity:
Query Match:
DB:
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      .022 CGCACGCCAGAGGTTGCCCGCAGTCGCCCACCCCCGTTATTGGATTTGATCATGGCAGCG 1081
                                    LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320
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Sequence 6, Application US/09866379

Patent No. 685365

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: BHORT, Jay

APPLICANT: GRETZ, Keith

APPLICANT: GRRETT, James

APPLICANT: GRRETT, James

APPLICANT: GRRETT, James

APPLICANT: OF INVERTION Nelson

APPLICANT: OF INVERTION NUMBER: US/09/866,379

CURRENT APPLICANTION NUMBER: US/09/866,379

CURRENT PILING DATE: 2001-05-24

PRIOR PILING DATE: 1999-05-25

PRIOR PELING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-35

PRIOR FILING DATE: 1999-05-318,528

PRIOR FILING DATE: 1999-05-31

PRIOR FILING DATE: 1999-05-31

PRIOR PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR PILING DATE: 1999-03-01

PRIOR PILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

SOPTWARE: PALENTIN VUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOPTWARE: PALENTIN VUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 6

LEMEGTH: 1901

PRIOR FILING DATE: 1901

PRIOR FILING DATE: 1901

PRIOR FILING DATE: 1907-08-13
                                                          1082 TIGACGCCCCATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG
                                                                                                321 PhelleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
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Matches:
Conservative:
Mismatches:
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2221.00
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LOCATION: (1)..(1901)
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                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                Gaps:
                                                                         4.81e-225
2221.00
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/: 99.1%
96.5%
LENGTH: 1489
TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
     ; LENGTH: 1489
; TYPE: DNA
; ORGANISM: E8C)
US-10-266-041A-9
                                                                              Alignment Scores:
Pred. No.:
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1328 CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1387
                                                                                             Squence 2, Application US/09715477

Patent No. 6441370

GENERAL INFORMATION:

APPLICANT: Lei, Xingen

TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE

FILE REFERENCE: 19603/4031

CURRENT APPLICATION NUMBER: US/09/715,477

CURRENT PALIAG DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/166,179

PRIOR FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 9

SOFWARE: Patentin Ver. 2.1

SEQ ID NO 2.
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	848 AAGTGAGCCCGACAATGTTTCATTAACCGGTGCGGTAAGCCTCCATCAATGCTGACGCGTGCGGTTAACCGGTGCGGTGCGGTTAAGCTCAATGCTGACGCGTGCGGTGCGGTAAGCTCAATGCTGACGCGTGCGGTTAAGCTGACGCGGTGCGGTGTAAGCTGCGGGGAATGCCCGGAGCGGGGGGGAAGCACACGGGAATGCCGGAGCGGAAATGCCGGAAGCAAACACACAC	Oy 261 A8DSETTISCHITTPARTITION	321 PheilealaGlyHisaspThrasnLeualaasnLeuGlyGlyAlaLeuGluLeuAsnTrp	361 ArgArgLeuSerAspAsnSerGlnTrplleGlnValSerLeuValPheGlnThrLeuGln	Qy 401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420 Db 11388 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTGTTCGTTGGCCGGTTTTACGCAA 1447 Qy 421 IleValAsnGluAlaArgllePrcAlaCysSerLeu 432 Db 1448 ATCGTGAATGAGCGCATACCGCGTTTTC 1483	RESULT 13 US-09-715-477-4 I US-09-715-477-4 Sequence 4, Application US/09715477 Sequence 4, Application US/09715477 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE FILE REFERENCE: 19603/4031 CURRENT PILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/166,179 PRIOR FILING DATE: 1999-11-18 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4 LENGTH: 1486 TYPE: DAM CREANISM: Escherichia coli

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Percent Similarity:
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Query Match:
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GENERAL INCEMATION:
GENERAL INCEMATION:
APPLICANT: KRETZ
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: 1425 Executive Square, Suite 1400
CITY: La Jolla & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla & Richardson P.C.
STREET: 12097
COUNTRY: US
COMPUTER: READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM FC compatible
OMPUTER: IBM FC compatible
OMPUT
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; Patent No. 5876997
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IMMEDIATE SOURCE:
CLONE: PHYTASE
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STRANDEDNESS: double
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367 CAGCGCACCGTCGCCACCGCGCAGTTCTTTATCACCGGCGTTCCCGGGCTGCGGCATC 426
                                                                                                 GlyvalCysGlnLeuAspAsnAlaAsnValThrAspAlaIle---LeuSerArgAlaGly 171
                                                                                                                                                                                                                       LeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspAsnValSerLeuThrGly 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 AlaTyrGlyValThrLeuProThrSerValLeuPheIleAlaGlyHisAspThrAsnLeu 329
              GluargThrargLysThrGlyGlualaPheAlaAlaGlyLeuAlaProAspCysAlaIle 132
                                                                                                                                                                                                  GlySerlleAlaAspPheThrGlyHisArgGlnThrAlaPheArgGluLeuGluArgVal 191
                                                                                                                                                                                                                                                               LeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSer 211
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                                                                                                                                                            GACGACTCCCCGGCGTTTCGCGAGAAAGCGCTGCAGGGGGAATGGAAAAAAGAGCGCCAGGGA
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Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPRENCE: 2709.200401
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 341
                                                                                                                                                                                                                                                                                                            CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 1149
                                                                                                                       ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380
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| CTGGTGACCAGCGGCGAGTGCCCGCAAAACGCGGTTTATGCCTACGCTAACACCCTG 366
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ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp
                                                                               ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGAACTGGTGTTTGAACGCTGG
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ORGANISM: Klebsiella pneumoniae
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Best Local Similarity:
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US-09-489-039A-341
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AAC88885;
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         GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
                                             - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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                                                      Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from
                                                                                                                                                                      The present sequence encodes a phytase enzyme from Escherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate in phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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WPI; 2001-112081/12
P-PSDB; AAB37892.
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                                                                                                       The present invention relates to novel dietary aids comprising sustained release biocompatible composition which comprises an agent (enzymes such as phytase, amylatas, esterase, protease) that assists in digestion. The biocompatible composition is effective upon oral consumption and release in the digestive tract of a subject. The dietary aids are useful for delivaring enzymes, therapeutics, medicine and agents to an organism. The use of enzymes and other agents in digestive aids of livestock or domesticated animals not only improves the animal's health and life expectancy but also assists in increasing the health of livestock or the production of foodstuffs from livestock. The present sequence is
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                                  New dietary aids comprising sustained release biocompatible compositions, comprise agent that assists in digestion, useful for delivering enzymes, therapeutics, medicine or agents to an organism.
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The patent discloses recombinant bacterial phytase from Bscherichia colicity apply phytase. The enzyme has phytase activity and improved processes to tabeance when compared with wild-type phytase. It has improved procease tability at low pH. The recombinant phytase is useful for improving the recombinant phytase is useful for improving the untritional value of phytate-containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are also used for generating recombinant digestive system life forms, for producing or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of environmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral supplements, enzymes or therapeutic drugs for animals from the dealty feed thus increasing the amount calories and nutrients present in the feed.
                                                                                                                                                                                                                             New bacterial phytase for e.g. improving the nutritional value of phytate containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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Phytase; ds; gene; phytate; appA gene; animal feed; inorganic phosphate; digestion enhancement; transgenic; thermal tolerance; protease stability
                                                                                                                                                                              Garrett JB;
                                                                                                                                                                             Gray KA, Barton NR,
                            location/Qualifiers
                                             /product= "Phytase"
                                                                                           13-AUG-1997; 97US-00910798.
01-WAR-1999; 99US-00259114.
13-APR-1999; 99US-00291931.
25-WAY-1999; 99US-00318528.
25-WAY-2000; 2000US-00580515.
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Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing gestion in humans and animals.

Claim 2; Fig 1; 62pp; English

The invention relates to an isolated Escherichia coli polymucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from W688. Q84W, A95P, K97C, 8168E, R180Y, N25CC or Y277D. Also included the E. coli appA gene ADA19491 (or an oligonucleotide derived from it) or its mutant sequence ADA19422, expression vectors, onest cells, a method of improving nutritional value of a phytate-containing foodstuff by contacting the phytate-containing foodstuff by contacting the phytate-containing andicordal phytase enzyme mutated phytase (where the phytate in the phytate-containing a microbial phytase (comprissing culturing the plant cell, plant part or plant under conditions where the nucleotide sequence is expressed and converting the plant cells, plants or plants or plants or plants or plants or animals (composition for animals (composition) an expension an expressed on disease an expension an expressed on system which expresses a nucleotide sequence contain an expressed on system which expresses a nucleotide sequence contain an expressed on system which expresses a nucleotide sequence comprising a phytase enzyme, a transgenic plant which is modified to contain an expressed on system which expresses a nucleotide sequence compusing phytase activity. The phytate enzyme is useful for improving the having phytase activity. The phytate enzyme is useful for improving the invented method end different or in humans and animals. The invented method end end of phytate-containing foodstuff, in the production of invented method end ended envented ended e invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence encodes E. coli B wild-type phytase.

Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;

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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease is stability at low pH. The phytase enzyme can be used in foodsuuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially significant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase tincorporated in to the dietary aid is safe for animals. The present sequence is Bscherichia coli B phytase DNA.
                             Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
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25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00586152.
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MATHER E J.
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KRETZ K.
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                                                                                                                                                                  CGTCGCCTAAGCGATAACAGCCAGTGGATTCAGGTTTTCGCTGGTCTTCCAGACTTTACAG
                         541 CGSCAAACGGGGTTTCGCGAACTGGAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGC
                                                                       LeulysArgGlulysGluSarCysSerLeuThrGlnAlaLeuProSerGluLeu
                                                                                                    CTTAAACGTGAGAAAACGGAGGAAGCTGTTCATTAACGCAGCATTACCATCGGAACTC
                                                                                                                                                                                                                                                                                                AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln
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ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                                                                               LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
                                                                                                                                                                                                                                                                                                                                                                       ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla
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ds; coding sequence; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture; osteoporosis; osteopathic; food.
                                                                                      E. coli B phytase coding sequence SEQ ID NO: 1.
                                                                     (first entry)
                                                                                                                                         Escherichia coli B.
                                                                     23-FEB-2006
                          RESULT 6
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Location/Qualifiers 1. .1323 /*tag= a /product= "Phytase"

Sequence 1323 BP; 323 A; 353 C; 357 G; 289 T; 0 U; 1 Other;

40000

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

3.15e-202 2302.00 100.0% 100.0% 100.0%

Best Local Similarity: Query Match:

Percent Similarity:

Alignment Scores:

US-10-601-319-2 (1-440) x AEE75412 (1-1323)

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The present sequence is that of a polymucleotide encoding the Escherichia coli B phytase. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, where the polypeptide is a modified sequence (AES75419) and the thermal tolerance maryer, comprising a series of mutations, improves the thermal tolerance carearyme, comprising a series of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition; a kit; an immobilized phytase; a fertilizer or soil additive; a liquid supplement for preventing muscle cramps; a chydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing collution and increasing nutrient availability in an environment or environment sample by degrading environmental phytic acid. The novel caryme is a dietary supplement useful for treating, preventing or cerversing osteoprosals or bone loss, and preventing muscle cramps. The cliquid supplement is useful for preventing muscle cramps. The cliquid supplement or environmental phytic caid, where the environment or environmental phytic acid, where the environment or environmental sample comprises a soil or a caid, where The immobilized phytase is useful in foodstuffs for improving the feeding value of phytate rich ingredients.
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214. .216
/*tag= b
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, Zorner P;
                                                                                                                                                                      13-AUG-1997; 97US-00910798.
01-MAR-1999; 99US-00259214.
13-ARR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
                                                                                                                                      01-SEP-2004; 2004US-00933115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Short JM, Kretz KA, G
Baum W, Robertson DE,
                                                                                                                                                                                                                                                                                          SHORT J M.
KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
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                                                                                                                                                                                                                                                                                                              (KRET/)
(GRAY/)
(BART/)
(GARR/)
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(BAUM/)
(ROBE/)
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us-10-601-319-2.rng

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1. .1323
/ttag= a
/product= "Mutant phytase enzyme"
214. .216
                                                                                                                                                                                                                                    Escherichia coli W phytase 875PH2 mutant DNA
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/*tag= c
replace (527,A)
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replace(893,T)
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01-MAR-1999; 99US-00259214.
13-APR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
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replace(895,G)
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P-PSDB; ADO50292, ADO50304.
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BARTON N R.
GARRETT J B.
O'DONOGHUE E.
MATHER E J.
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KRETZ K.
                                                                                                                                                                                                                                                                                        Escherichia coli.
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                                                                                                                    ThrTrpProVallysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80
                                                                                                                                                             GlyHisTyrGlnArgClnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100
                                                                                                                                                                            SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160
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                                                                                         AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140
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                                      PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40
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         TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCACACTCGTCATGGT
                                                                              ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
                                                                                                                                                                                                                                                                                                                                           AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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 MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla
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Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
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Disclosure; Page; 74pp; English.

The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expression of the mucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease catability at low ph. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme and fishes, commercially commercially and and and and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as plyg, goats, laboratory rodens, commercially significant avian species such as Ghicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially making and baking, in dietary aids for animals. The method provides easy manufacture of the active indicater. The phytase composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present sequence is Becherichia coll w phytase mutant DNA. Note: The present sequence is not shown in the specification but has been derived from the sequence is solventy.

Sequence 1323 BP; 324 A; 353 C; 356 G; 289 T; 0 U; 1 Other;

	1323	436	-	3	0	0
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	2.2e-200	2282.00	99.3\$	7: 99.18	99.18	12
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

US-10-601-319-2 (1-440) x ADO50303 (1-1323)

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oginsera	rarghis6	palaTrpP	ealafyrL	aGlyCyaPro	eThrGlyG	nAlaAspT	uAspAsnA	eThrGlyH
							:	
GCAATCTG	rccrcarg	cccarcc	ccctarc	GGGCTGCCCG	AACAGGCG	GGCAGATA	GGATAACT	TACCGGGC
MetlysalaileleuileProPheleuSerLeuleuileProLeuthrProGinSerala	PhealaginSergiubrogiubeuLysbeugiuSerValVallileValSerargHisgly	ValargalaprothriyaalathrGlnLeumetGlnAspValthrProAspAlatrpPro	TheTeppeovallysbeuglyTepleuThePoargGlyGlyGluleuIlealaTyrleu	Glyhistyrchargchargleuvalalaaspchyleuleualalyshysglycyspro	Ginsergiyginvalalaileilealaabpvalabpgiuargthrargiysthrigiygiu	AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr	SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla	ABNVAIThrAspAlaileLeuSerArgAlaGlyGlySerileAlaAspPheThrGlyHis
LeuilePr	Servalva	GlnAspva	ArgGlyGl	GlyLeule	Aspgluar		Threlyva	Glyseril
CTGATTCC	\AGTGTGGT	GCAGGATGT	scgnggrgg	GGATTGCT	Gacgagcg		ACTGGCGT	GGGTCAAT
LeuserLei	Lysteuglu	31nLeumet	LeuThrPro	Valalaasi	Alaaspva]	AspCysAle	ProLeuLys	Argalagly
FTATCTCT	AAGCTGGAA	CAACTGATC	TGACACC	STAGCCGAC	3CrGargr		CTCTAAAA	AGGCCAGG
leProPhe	roGluLeul	yaalaThr	euGlyTrp	InArgleu'	laileile	eualapro/	euPheasn	leteuser/
cccartr	CGGAGCTG	AGGCCACG	rGGGrrGG	AGCGTCTG	CGATTATT	rGGCACCT	TATTTAAT	TCCTCAGC
alleLeul	nSerGluP	aProThrL	ovallysl	rglnargg	yGlnvala	aAlaGlyL	OASPProL	raspalai
GATCTTAA	GAGTGAGC	TCCAACCA	GGTAAAAC	ccaacgcc	rcaggres	cccccccc	CGATCCGT	TGACGCGA
MetLysa] argaaag	PheAlaGl	valArgAl GTGCGTGC	ThrTrpPr Accreecc	Glyhisty GGACATTA	GlnSerGl CAGTCTGG	AlaPheAl GCCTTCGC	SerSerPr TCCAGTCC	AsnvalTh
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme in the yeast. The invention also relates to establisty at low pil. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytase rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially significant avian species such as Chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commostion, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present incorporated in to the dietary aid is safe for animals. The present sequence is Rangaroo rat Escherichia coli phytase mutant DNA. Note: The present sequence is shown in the specification but has been derived from Escherichia coli bhytase DNA ADOSO291.
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'note= "Encodes Arg"
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                             /*tag= c
replace(893,T)
/*tag= d
replace(895,G)
/*tag= e
replace(934,G)
/*tag= f
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01-MAR-1999; 99US-0025214.
13-APR-1999; 99US-00291331.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
                 replace (527, A)
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(GART) BARTON N R.
(GARN) GARRETT J B.
(ODON) O'DONGETUE E.
(MATH) MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-374952/35.
P-PSDB; ADO50302.
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                                                                                                                                                                                                                                                                                                                                                                                     SHORT J M.
KRETZ K.
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GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysGlyCysPro

181 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC 240

ThrTrpProVallysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu

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121 361 141

GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu

AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr

GCCTTCGCCGCCGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 421 TCCAGTCCCGATCCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG AsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180

191

181 541 201

481 AACGTGACTGACGCGATCCTCAGCAGGGCAGGGTCAATTGCTGGCTTTACCGGGCAT

540 200 9 220 9 240

ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro

PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly

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ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA

MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla

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LeulysArgGlulysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
                                 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                              LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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Length:
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                                       61 TTGGTTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCGTGGT
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                                                                            CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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/product= "Phytase associated protein"
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P-PSDB; AAU7775.
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Best Local Similarity:
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense conding a polypeptide whose expression is inhibited by the antisense collypeptide or its fragment whose expression is inhibited by the antisense collypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide of specifically binding the polypeptide of specifically binding to proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound's activity; (1) a cullure comprising strains in which the gene compound's activity; (11) a cullure comprising strains in which the gene compound's activity; (11) a cullure comprising strains in which the gene compound's activity; (11) a cullure comprising strains in which the gene to which each of the strains is present in a culture or collection of
                                       CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCGGAGAGGTGAAACTGACC 1200
                                                                                                                                                                     LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to an isolated nucleic acid comprising any one of
GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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Xu HH;
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Forsyth RA,
                                                                                                                                                                                                                                                           432
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-WAR-2002; 2002US-0362699P.
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Trawick JD,
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P-PSDB; ABU15427.
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strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGTCTGGTCAGGTCGCGGATTATTGCTGATGTCGACGACGACGTACCCGTAAAAACAGGCGAA 360
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AppA phytase; modified phytase; K-12; animal feed; feed additive; phosphorus; phytate; myo-inositol hexakisphosphate; food production; wet grain milling; dental care product; bone resorption; osteoporosis; osteopathic; kidney stone; metal removal; waste treatment; cleaning product; rust removal product; gene; ds.
                                               GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCCAATTTTATTTGCTACAA
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                                                                            ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAgpLeu1leMetAlaAla
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/product= "AppA phytase"
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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The invention relates to recombinant modified AppA phytases having

modified phytase activity. The AppA phytases are derived from a mature

Escherichia coll AppA phytase designated EBC1825 (see AbL16120), and

comprise subsitutions at least one of residues 26, 43, 46, 54, 73, 113,

CC 26, 184, 228, 384 or 410, or at a residue located within 5 residues of

those listed above. The invention also encompasses polymucleotides

concoding a modified AppA phytase and which further encodes a secretion

signal sequence operable in Bacillus subtiliss) comprising the

colymucleotide sequences; and a method for the production of the modified

AppA phytases. The invention also discloses a method of producing an

colympetide having phytase activity; a method of producing a heterologous

colympetide having phytase activity; a method of producing a neterologue

colympetide having phytase activity; a method of producing a neterologue

colympetide having phytase activity; a method of producing a neterologue

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colympetide having phytase activity; a method of producing a neterologue

colympetide having phytase activity; a method of producing a neterologue

colympetide having phytase are useful as an animal feed additive,

particularly in feeds for non-ruminant livestock such as pigs and poultry

which lack the digestive enzymes for extracting phosphorus from phytase

contains poters proceed phosphorus. The modified AppA phytases also have

many other agricultural, industrial, medical and nutritional

applications For example, they can be used in the isolation and

recovery of rare metals to produce lower phosphate homologs of phytate,

which may be used in toothpaste and other dental care products as well as

collennial treatments or preventatives of bone resorption (e.g., in

clear, tofu and nutritional supplements); in wet grain milling; percentions

clearing, percentages. The modified
                                                                                                                                                                                                                                                                            Novel recombinant phytase having modified phytase activity comprising modification of amino acid residues in mature Escherichia coli phytase designated EBC18B2, useful as feed additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents Escherichia coli strain K-12 AppA phytase
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Schellenberger
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GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100
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The patent discloses recombinant bacterial phytase from Escherichia colicity and Apptase. The enzyme has phytase activity and improved thermal colerance when compared with wild-type phytase. It has improved thermal tolerance when compared with wild-type phytase. It has improved protease stability at low pH. The recombinant phytase is useful for improving the nutritional value of phytate-containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are also used for generating recombinant digestive system life forms, for producing or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of environmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed. The present sequence is a DNA encoding B. coli appA phytase wild type protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
                                                                                                                                                                                                                                             Bacterial phytase, K12 appA phytase; protease stability; anabolic; gastrointestinal; untritional value; feed treatment process; therapy; thermal tolerance; growth performance; alcoholic drink; biopulping; non-alcoholic drink; biobleaching; ds.
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                                                                                                                                                              Escherichia coli appA phytase wild type DNA
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AAD25463;
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U; 1 Other;

499 G; 428 T; 0

BP; 474 A; 499 C;

Sequence 1901

1901 430 0 2 0

Conservative: Mismatches: Indels: Gaps:

(1-1901)

x AAD25463

Length: Matches:

7.83e-196 2235.00 99.5% 99.5%

Similarity:

1387

420

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1388 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGCATGTTTTCGTTGGCAGGTTTTACGCAA 1447
                                                                                                                                                                                                                                                                                                         Phytase; ds; gene; phytate; appA gene; animal feed; inorganic phosphate; digestion enhancement; transgenic; thermal tolerance; protease stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated Bscherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from W68E, Q84W, A95P, K977C, S168E, R180V, N226C or Y277D. Also included the E. coli appA gene ADA19449 (or an oligonucleotide derived from it) or its mutant sequence ADA19452, expression vectors,
GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                            CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                                   LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing digestion in humans and animals.
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                                                                                                                                                ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1483
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188. .1486
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/product= "Phytase"
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01-WAR-1999, 99US-00259114.
13-APR-1999, 99US-0021931.
25-WAY-1999, 99US-00318528.
25-WAY-2000, 2000US-00580515.
                                                                                                                                                                                                            standard; DNA; 1901
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KRETZ K A.
GRAY K A.
GARRET J B.
O' DONOGHUE HATHUR E J.
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P-PSDB; ADA19450.
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                                                            TTCGCTCAGAGTGAGCCCGGAGCTGAAGCTGGAAAGTGTGGTGATGTCACAGTCGTCATGGT
                                                                                            ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
                                                                                                            GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
                                                                                                                                           ThrTrpProVallysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
                                                                                                                                                                  ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC
                                                                                                                                                                                           GlyHisTyrGlnArgClnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro
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                                              PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
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containing foodstuff by contacting the phytate-containing foodstuff with containing foodstuff by contacting the phytate-containing foodstuff with a pure as pure phytase enzyme mutated phytase (where the phytate in the phytate.) The phytate enzyme catalyzes the liberation of inorganic phosphate from the phytate in the phytate. Containing foodstuff), a method to produce an animal feed containing a containing the plant call, plant part or plant under conditions where the nucleotide sequence is expressed and converting the plant cells, plants or plant into a composition for animal converting the plant seeds, plant of feed), a feed composition for animals (comprising the plant seeds, plant of converting the plant cells, plant parts or plants in admixture with a phytase enzymes foodstuff), a method to treat a human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzymes or comprising administering to the human or animal the plant seed, plant cells, plant parts or plants of a transgenic plant which is modified to contain an expression system which expresses a nucleotide sequence or encoding a phytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a phytase activity. The phytate enzyme is useful for improving the nutritional value of phytate enzyme is useful for improving the nutritional value of phytate enzyme is useful for improving the invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence represents the E. coli K12 appA gene encoding wild-type phytase.

Sequence 1901 BP; 474 A; 499 C; 499 G; 428 T; 0 U; 1 Other;

AlaPheAlaAlaGlyLeuAlaProAspCygAlaIleThrValHisThrGlnAlaAspThr 140 160 180 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 247 367 487 GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120 607 667 427 GlyHisTyrGlnArgGlnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100 181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200 40 80 ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGGTGATCGCCTATCTC GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGACGACGTACCCGTAAAACAGGCGAA SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla MetLysAlalleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu AsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrGlyHis PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly Length: Matches: Conservative: Mismatches: Indels: Gaps: US-10-601-319-2 (1-440) x ADA19449 (1-1901) 7.83e-196 2235.00 99.5% 99.5% 97.1% Best Local Similarity: Percent Similarity: Alignment Scores: 188 248 21 41 308 61 898 81 428 488 121 548 608 161 101 141 Query Match: DB: . No.: ద ò 8 8 8 8 8 8 6 B 6 B 6 B 6 B 6 B

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                                                            CTTAAACGTGAGAAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                                                LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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                                                                                                                                                                                                                                                                                                                                                                     The invention discloses a new isolated or recombinant nucleic acid which encodes a polypeptide having a phytase activity. Also claimed is a nucleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the public acid, an antisense oligonucleotide, inhibiting the polypeptide and a second domain, an array comprising immobilised polypeptide and a second domain, an array comprising an antibody that specifically binds to the polypeptide, a food supplement for an animal, an edible enzyme delivery an edible pellet comprising a granule edible enzyme delivery matrix, an edible pellet comprising a granule edible carrier and the polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, matring whether a compound blunds to the polypeptide, carrier and the polypeptide, matring whether a compound blunds to the polypeptide, comprising a composition, a soybean meal, isolating or identifying the polypeptide, matring whether a compound blunds to the polypeptide, comprised to the phytase polypeptide to enzymatic inactivation in a digestive system and processing of corn and sorghum kernels. The phytase cor inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or encoding the Bacherichia coll apph phytase.
                                                                                                                                                                                                                                                                                              * nucleic acid encoding a polypeptide having phytase activity, useful
improving the feeding value of phytate rich ingredients or as an aid
phytate digestion.
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                                                                                        13-AUG-1997; 97US-00910798.
01-MAR-1999; 99US-00259214.
13-APR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00586515.
24-MAY-2001; 2001US-00866379.
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            US2003103958-A1
                                                                24-MAY-2002;
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Mathur EJ;
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal colerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in dist of numerous animals including mammals, fools and fishes, commercially significant mammals such as plgs, goats, laboratory rodents, commercially significant avian species such as chicken, ducks, doves, parrot, etc.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
                                                                                                                                                            AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; gene; ds.
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/product= "AppA phytase"
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GARRETY J B.
O'DONOGHUE E.
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commercially farmed fish such as guppy, zebrafish, molly, swordtail, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase incorporated in to the dietary aid is safe for animals. The present sequence is Escherichia coli K12 appA phytase DNA.
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        LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
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AR127818 Sequence
AR130956 Sequence
                                                                                                               June 14, 2006, 10:58:44; Search time 5255.78 Seconds (without alignments) 8030.264 Million cell updates/sec
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                GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                               - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Short, J.M. and Kretz, K.A.
Recombinant bacterial phytases and
Patent: US 6183740-A 1 06-FEB-2001;
Location/Qualifiers

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Kretz,K.
Phytase
Patent: US 6190897-A
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GluilePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArglleThr LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr Length: Matches: Conservative: Mismatches: Indels: Gaps: DNA" 20-FEB-2001; US 6190897-A 1 20-FEB-200
Location/Qualifiers
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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Short,J.M. and Kretz,K.A.
Recombinant bacterial phytases and use
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Unclassified.
1 (bases 1 to 1323)
Short,J.W., Kretz,K.A., Gray,K.A., Barton,N.R., Garrett,J.B., O'Donoghue,E. and Mathur,E.J.
Recombinant bacterial phytases and uses thereof Patent: US 6855365-A 1 15-FEB-2005,
Diversa Corporation; San Diego, CA
Location/Qualifiers
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Enterobacteriaceae, Escherichia.
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Enterobacteriaceae; Escherichia.
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Recombinant bacterial phytases and uses thereof Patent: WO 0190333-A 1 29-NOV-2001;
DIVERSA CORPORATION (US)
Location/Qualifiers
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Sequence 1 from Patent WO0190333.
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	Qy 401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420	RESULT 9 AR636190 AR636190 LOCUS LOCUS DEFINITION Sequence 7 from patent US 6855365. ACCESSION AR636190.1 GI:62768873 KEYWORDS SOURCE UNKNOWN.	ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1901) AUTHORS Short,J.M., Kretz,K.A., Gray,K.A., Barton,N.R., Garrett,J.B., O'Donoghue,E. and Mathur,E.J. TITLE Recombinant bacterial phytases and uses thereof JOURNAL Patent: US 6855365-A 7 15-FEB-2005; Diversa Corporation; San Disego, CA	FEATURES Location/Qualifiers 11. 1901 /organism="unknown" /mol_type="genomic DNA"	Alignment Scores: 2.74e-198 Length: 1901 Score: 2235.00 Matches: 430 Percent Similarity: 99.5\$ Mismatches: 2 Query Match: 97.1\$ Indels: 0 DB: 2 daps: 0	10-601-319-2 (1-440) x AR636190 (1-1 1 MetLysAlaIleLeuIleProPheL 	Oy 21 PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40	Oy 61 ThrTrpProValLySLeuGlyTrpLeuThrProArgGlyGlyGlyGluLeuIleAlaTyrLeu 80
Score Similarity 100.0\$ Matches 440	1 Valargala ProThrLysalaThrGlnLeuwetGlnAspValThrProAspAlaTrpPro	Qy 81 GlyHisTyrGlnArgClnArgLeuValAlaAspGlyLeuLeuAlaLysLysGlyCysPro 100 Db 241 GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG 300 Qy 101 GlnSerGlyGlnValAlaIleIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120 Db 301 CAGTCTGGTCAGGTCGCGATTATTGCTGAAGGCGTACCGTAAAACAGGCGAA 360	21 61 41	161 AsnValThrAspAlaIleLeuSerArgAlaGlyGlySerIleAlaAspPheThrClyHis	Oy 181 Argentary presented the control of the contr	Qy 221 LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln	Db 841 CGCACGCCAGAGGTTGCCCGCGCGCCCCCTTATTGGATTTGATCATGGCCAGCG 900 Qy 301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValleu 320

Garrett, J.B. and

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LeulysArgGlulysGluAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220
                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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O'Donoghue,E.
Recombinant bacterial phytases and uses thereof
Patent: WO 0190333-A 7 29-NOV-2001;
DIVERSA CORPORATION (US)
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Ostanin,K. and Van Etten,R.L.
Asp304 of Escherichia coli acid phosphatase is involved in leaving
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299. .301
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                                                       .. Chem. 268 (28), 20778-20784 (1993)
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 CITAAACGIGAGAAACAGGACGAAGCIGIICAITAACGCAGGCAITACCAICGGAACIC 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bscherichia coli periplasmic phosphoanhydride phosphohydrolase (appA) gene, complete cds.
MS8708
                                                             GAGATATTTCTCCTGCAACAAGACACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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J. Biol. Chem. 267 (32), 22830-22836 (1992)
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                                                                      LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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/db xref="texon:32630"
/noTe="R15/APPA transgene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | State | Age, | State | State
                                                                                                                                                                                                                                 Standard name="D304B mutant"
| Standard name="D304B mutant"
| note="created by site directed mutagenesis" |
| citation=[3] | citation=[3] |
| phenotype="Asp 304 changed to Glu" |
| replace="gag" |
| 1497. . 1522 |
| sense = "appA" |
| note="rho-independent terminator"
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/organism="lunasigned DNA"
/db_xref="taxon:32650"
/note="R15/APPA plasmid with pBLCAT3 vector"
    linear
                                                                                                   Forsberg, C.W., Golovan, S. and Phillips, J.P.
Transgenic animals expressing salivary proteins
Patent: WO 0064247-A d O.2-NOV-2000;
UNIVERSITY OF GUBLPH (CA)
Location/Qualifiers
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Best Local Similarity: 99.5% Mismatches: 2 Query Match: 27.1% Indels: 0 DB: 2 Gaps: 0 US-10-601-319-2 (1-440) x AX042373 (1-6708)	MetLysAlalleLeulleProPhe 	Qy 21 PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40	Qy 41 ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	Oy 61 ThrTrpProValLysLeuGlyTrpLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80	Qy 81 GlyHisTyrGlnArgClnArgLeuValAlaAspGlyLeuLeuAlaLysGlyCysPro 100	Qy 101 GlnSerGlyGlnValAlaileilealaAspValAspGluArgThrArgLysThrGlyGlu 120	Oy 121 AlaPheAlaAlaGlyLeuAlaBrOASpCySAlaIleThrValHiSThrGlnAlaASpThr 140	Oy 141 SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160	Qy 161 AsnValThrAspAlaIleLeuSerArgAlaGlyGlyGlySerIleAlaAspPheThrGlyHis 180 2291 AACGTGACTGACGGATCCTCAGCAGGAGGACGAGGTCAATTGCTGACTTACCGGGCAT 2350	Oy 181 ArgGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200	Oy 201 LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220	221 Lysvalderniahbhashvalderleuntstynlavalderleuniat	Qy 241 GluilePheLeufeuGinGlnAlaGinGlyMetProGlyTrpGlyArgileThr 260	Oy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280	Qy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla 300	Oy 301 LeuThrProHisProFroGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320	321 Phellealdiylishsphrashleualadshleudlydlyalateudluchashrrp 340
Db 2411 CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC 2470 Qy 221 LysValSerAlaAspAsnValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	GluilePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArglleThr 	Oy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheTyrLeuLeuGln 280 	Qy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleMetAlaAla 300 Db 2651 CGCACGCCAGAGGTTGCCCGCAGCCGCCCCCTTATTAGATTTGATCAAGACAGCG 2710	Qy 301 LeuThrProHisBroProGlnlysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320 	Oy 321 PheilealaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	Qy 341 ThrLeubroGlyGlnProAspAsnThrProProGlyGlyGlubeuValPheGluargTrp 360 bb 2831 ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGGTGATTGAACGCTGG 2890	Qy 361 ArgArgLeuSerAspAsnSerGlnTrplleGlnValSerLeuValPheGlnThrLeuGln 380 	Qy 381 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400	Qy 401 LeualaGlyCysGluGluargAsnalaGlnGlyMetCysSerLeualaGlyPheThrGln 420 	Qy 421 IleValAsnGluAlaArgIleProAlacysSerLeu 432 	RESULT 15 AX042373 LOCUS AX042373 LOCUS AX042373 FOR Patent WO0064247.		_	AUTHORS Foreberg, C.W., Golovan, S. and Phillips, J.P. TITLE Transgenic animals expressing salivary proteins JOURNAL Patent: WO 064247-A 2 02-NOV-2000; UNIVERSITY OF GUELPH (CA)	FEATURES Location/Qualifiers source 16708 /organism="synthetic construct" /mol_type="unassigned_DNA"	<pre>/db xret="taxon:32630" /note="R15/APPA + intron plasmid with pBLCAT3 vector" ORIGIN</pre>	Alignment Scores: 1.72e-197 Length: 6708 Pred. No.: 2235.00 Matches: 430 Percent Similarity: 99.5* Conservative: 0

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Search completed: June 14, 2006, 13:53:05 Job time : 5289.78 secs

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OM protein - protein search, using sw model

June 13, 2006, 10:22:24; Search time 25.7339 Seconds (without alignments) 1645.118 Million cell updates/sec Run on:

Title: Perfect score:

US-10-601-319-2 2302 1 MKAILIPFLSLLIPLTPQSA......IVNEARIPACSLRSHHHHHH 440 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMM	QI	B36733	H90770	D85633	AC0201	F90773	B85636	S25627	JV0087	E87316	AG0632	206167	T16058	A33395	S14742	JH0610	B89130	TVFF7L	T30225	A56925	A54429	BVECSC	852250	AC0304	A29440	C81716	JN0890	H75530	C85535	
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	Query Match	97.1	96.0	96.0	41.0	23.7	23.7	23.5	23.4	22.8	22.8	6.1	5.8	5.7	5.3	5.1	4.9	4.7	4.7	4.7	4.6	4.6	4.6	4.5	4.4	4.4	4.4	4.4	4.4	
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ALIGNMENTS

RESULT 1
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N'Alternate names: phosphoanhydride phosphohydrolase, periplasmic: phytase 6
C;Species: Bscherichia coli
C;Date: 19-Apr-1991 #sequence revision 19-Apr-1991 #text change 09-Jul-2004
C; Accession: B36733; S18018; B64839; A26534; S17960; S33278
R; Dassa, J.; Marck, C.; Boquet, P.L.
J. Bacteriol. 172, 5497-5500, 1990
A; Title: The complete nucleotide sequence of the Escherichia coli qene appA revea
A; Reference number: A36733; MUID:90368616; PMID:2168385
A; Accession: B36733
A;Status: preliminary
A; Molecule type: DNA
A; Residues: 1-432 < DAS>
A; Cross-references: UNIPROT: P07102; UNIPARC: UPI000004750A; GB: M58708; NID: q145283
R; Greiner, R.; Jany, K.D.

als sign

3; PIDN

Biol. Chem. Hoppe-Sayler 722, 664-665, 1991
A;Title: Characterization of a phytase from Escherichia coli.
A;Reference number: S18018
A;Accession: S18018
A;Molecule type: procein
A;Residues: 23-13 <GRE>

A;Cross-references: UNIPARC:UP10000179815
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Status: nucleic acid sequence not shown; translation not shown

A;Ratious: nucleic acid sequence not shown; translation not shown

A;Residues: 1-432 < SELAT>

A;Residues: 1-432 < SELAT>

A;Cross-references: UNIPARC:UPI000004750A; GB:AE000200; GB:U00096; NID:g2367111; PIDN:AA

A;Experimental source: strain K-12, substrain MG1655

B;Touati, B.; Danchin, A.

Biochimie 69, 215-221, 1987

A;Title: The structure of the promoter and amino terminal region of the pH 2.5 acid phos

A;Reference number: A26534; MUID:87271766; PMID:3038201

A;Accession: A26534

A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-17 <DA2>

A;Cross-references: UNIPARC:UP1000016FFB1; GB:S63811; NID:g238656; PIDN:AAB20286.1; PID:

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119 GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT 178
                                       Query Match
Best Local Similarity 98.4%;
Matches 427; Conservative
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A,Molecule type: protein
A,Rolecule type: protein
A,Residues: 23-31,'A',33-34 <GR2>
A,Cross-references: UNIPARC:UPI0000179816
C,Comment: In addition to cAMP-mediated control, this enzyme is induced when bacterial naerobic conditions.
                                                                                                                              Genetics:
A;Gene: apph
A;Map position: 25 min
C;Keywords: monomer; periplasmic space; phosphohistidine; phosphoprotein; phosphoric c;Keywords: monomer; periplasmic space; predicted <SIG>F;1-22/Domain: signal sequence #status predicted <NAT>F;23-112/Product: acid phosphatase #status predicted <MAT>F;33-112/Product Arg #status predicted
F;39/Active site: Arg #status predicted
F;39/Active site: His (phosphohistidine intermediate) #status predicted
                            coli.
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R;Greiner, R.; Konietzny, U.; Jany, K.D.
Arch. Biochem. Biochyys. 303, 107-113, 1993
Arth. Biochem. Biochyys. 303, 107-113, 1993
A;Title: Purification and characterization of two phytases from Escherichia
A;Reference number: S33278; MUID:93256556; PMID:8387749
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Pred. No. 1.2e-171;
0; Mismatches 2; Indels
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Best Local Similarity
Matches 430; Conserva
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Cipecies: Escherichia coli
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Cipate: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
Cipate: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
Cipate: 10-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 09-Jul-2004
Cipate: 10-Peb-2001 #sequence_revision 16-Peb-2001 #s. Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grocbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.† Lile: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Racenson: D85633
A;Ratus: Preliminary
A;Ratus: preliminary
A;Ratus: preliminary
A;Residues: 1-444 <STO>
A;Cross-references: UNIPROT:QBXC29; UNIPARC:UPI0000165751; GB:AE005174; NID:g12514245; Pl
Cipateinental source: strain 0157:H7, substrain EDL933
Cipateinental
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   Length 434;
                                                                   Indels
                              Pred. No. 1.2e-169;
0; Mismatches 5;
   7
   8
Score 2210;
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PST/75 amic glucose-1-phosphatase [imported] - Escherichia coli (strain 0157:H7, substra periplasmic glucose-1-phosphatase [imported] - Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Escherichia coli (5.5pecies: Bacherichia coli (5.5peci
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85636
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
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          ERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSL-NTPPGEVKLTLAGCEERNAQGMCSLA
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                                                                                                           417 GFTQIVNEARIPACSL 432
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TPQKKVAKVIEPACHI 441
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Matches 135; Conservative
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acid phosphatase (EC 3.1.3.2) [imported] - Yersinia pestis (strain CO92)
C;Speciaes : Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0201
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. A: Parkhill, J.; Wurberford, R.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G.;
II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.; Whitehead, S.; Barrell, A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; WuID:21470413; PMID:11586360
A;Accession: AC0201
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-441 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:Q8ZFP6; UNIPARC:UPI0000DCCF7; GB:AL590842; PIDN:CAC90470.1; GGenetics:
A,Gene: YPO1648
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 APRELERVLNPPQSNLCLKREKQDESCSLTQALPSELKVSAD--NVSLTGAVSLASMLTE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 AGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 IFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAAL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHRQTAFRELERVLNFPQSNLCLNREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM
                                                                                                                                                                                                               LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM
                                                                                                                                                                                                                                                                                                             311 IALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVPE
                                                                                                                                                                                                                                                                                                                                                                               RWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGF
                                                                                                                                                                                                                                                                                                                                                                                                         GHRQTAFRELERVINFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM
                                                                                                                                                                                                                                                                              AALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFE
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41.0%; Score 943.5; DB 2; Length 4
Best Local Similarity 45.6%; Pred. No. 6.5e-68;
Matches 199; Conservative 66; Mismatches 156; Indels
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241 YYEGPPADQVAWGLVDTPEKMKKINTLKNAYQETLFTPKIIAKNVAHPIINYIDKGFVSV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 GCKVNIHHOPEIGKMDPVFNPIIT-----NGSPEFKOKALAAMDDYLKGLSLKAGYE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 DKGETA-----KFIFLVGHDSNIASLMSAMDFKPYQLAQQYEHTPIGGKLVFQRWTDK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 SDNSQWIQVSLVPQTLQQMRDKTPLSLNTPPGEVKLTLAGCE-ERNAQGMCSLAGFTQIV 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 QTKKDFMKVEYVYQTADQLRDNAYLSLETPPRHVTLELKDCPVDKN--GYCSWEDFQKVM 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 QAQGMP--EPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPH 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 PPOKQAYGVTLPTSVLFIAGHDTNLANLGGALELN-WTLPGQPDNTPPGGELVFERWRRL 363
                                                                                                                                                                      70 TPRGGELIAYLGHYORQRLVADGLLAKKGCPQSGQ-VAIIADVDERTRKTGEAFAAGLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELERVINFPQSNLCLKREKQDESCSJTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQ
                                                                                                                              10 SLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWL
            Local Similarity 30.5%; Pred. No. 1.3e-35; tes 129; Conservative 84; Mismatches 182;
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iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
Afritle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference preliminary
A; Reference preliminary
A; Residues: 1-413 < 870>
A; Residues: 1-413 < 870>
A; Cross-references: UNIPROT:Q8XBZ6; UNIPARC:UPIO000000533; GB:AE005174; NID:g12514273; F
A; Reperimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: agp
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C;Species: Species: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 ANRDLMKIEYVYQSAEQLRNADALTLQAPAQRVTLELSGC-PIDADGFCPMDKFDSVLNE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 AITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MP--EPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQK 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLNPPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.7%; Score 545; DB 2; Length 41:
32.1%; Pred. No. 6.18-36;
tive 76; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 32.13
Matches 135, Conservative
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C;Accession: JV0087; H64841

R;Pradel, B.; Marck, C.; Boquet, P.L.
J. Baquet, P.L.
A;Title: Nucleotide sequence and transcriptional analysis of the Escherichia coli agp ger A;Reference number: JV0087; MUID:90130318; PMID:2153660
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-413 - CRAA.
A; Residues: 1-413 - CRAA.
A; Cross-references: UNIPROT: P19926; UNIPARC: UPI00001256FB; GB: M33807; NID: G145217; PIDN: R;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617; PMID: 9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPARC:UDI00001256FB, GB:AE000202; GB:U00096; NID:g1787233; PIDN:AAC
A,Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: essential for growth in a high-phosphate medium containing glucose-1-phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: optimal at low pH
C;Keywords: homodimer; periplasmic space; phosphohistidine; phosphoprotein; phosphoric mc
C;Reywords: homodimer; periplasmic space; predicted <SIG>
P;1-22/Damain: signal sequence #status predicted <SIG>
P;23-413/Product: glucose-1-phosphates #status predicted <WAT>
P;40/Active site: His (phosphohistidine intermediate) #status predicted
F;311/Active site: His #status predicted
glucose-1-phosphatase (BC 3.1.3.10) precursor - Escherichia coli (strain K-12) C;Species: Escherichia coli (C;Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: H64841
A;Status: nucleic acid sequence not shown, translation not shown
A;Molecule type: DM
A;Residues: 1-413 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: agp
A,Map position: 23 min
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PIDN

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CiKeywords: periplasmic space; phosphohistidine; phosphoprotein; phosphoric monoester F1-29/Domain: signal sequence #status predicted <SIGS F30-417/Product: glucose-1-phosphatase #status predicted <MAT> F;42/Active site: His (phosphohistidine intermediate) #status predicted

Length 417;

DB 2;

23.5%; Score 541;

Query Match

F;314/Active site: His #status predicted

S

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Glucose-1-phosphatase precursor (GlPase), secreted [imported] - Salmonella enterica subsidiacies: Salmonella enterica subspecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: Ad6632
E;Parkhill, J; Dougan, G;; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant salmonella enterica serov A;Accession: Ad6632
A;Accession: Ad6632
A;Accession: DAA
A;Accession: DA
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                                                                                                                                                                                                                         WRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFT 419
                                                                                                                                                                                                                                                                                                                     80 LGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQAD 139
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                                                 177 EQLDALLMQCDKGPCPPAPGKRVFDAKPGFVDG--EBL-----AGLSGPEAFASGVTE
                                                                                                 IFILQQAQGMPEPGWG-RITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 RITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAYGVTLPT
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                                                                                                                                                                                             LTPHPPQKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPG-QPDNTPPGGELVFER
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B87316

periphasmic phosphoanhydride phosphohydrolase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87316
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87316
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-414 <STO>
A;Cross-references: UNIPROT:Q9AAQ4; UNIPARC:UPI00000C70A0; GB:AE005673; NID:g13421731; F
C;Genetics:
A;Gene: CC0542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MP--EPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQK 308
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                                                                                                                          71 PRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDC
                                                                                                                                                                                                                    VLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQG
                                                                                                                                                                                                                                                                                                                                                                                                                  352 ANRDLMKIEYVYQSAEQIRNADALTLQAPAQRVTLELSGC-PIDADGFCPMDKFDSVLNE
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                                                                                            13 IPLIPQSAFAQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAWPTWPVKLGWLT
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    Length 413;
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                                                 Indels
                                            75; Mismatches 181;
23.4%; Score 539; DB 2; 32.1%; Pred. No. 1.8e-35;
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Matches 148; Conservative
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135; Conserv
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A;Cross-references: UNIPROT:Q19390; UNIPARC:UPI000007AD42; EMBL:U40939; NID:g1072175; PII
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                                                                                328 YF---RNESDKAPWPLSLP-----GCPHR-----CPLQDFLRL-TEPVVPKDWQQE 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114
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A;Introns: 23/3; 59/3; 88/3; 138/3; 202/3; 244/1; 270/3; 312/3; 349/3; 377/1
C;Superfamily: mammalian acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Caenorhabditis elegans
Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 NDSVGDYHNELVMSYFETHLQKONSTKGV-----FISGHDTNLVTIWESLRLD----GH
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                                                                                                                                                                                    375 VFQTLQQMRDKTPLSLNTPPGGVKLTLAGCBERNAQGMCSLAGFTQIVNEARIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Fulton, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F13D11.
A;Reference number: S69020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F13D11.1 - Caenorhabditis elegans
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A; Residues: 1-423 < VONA
A; Cross-references: UNIPROT: P11117; UNIPARC: UP10000131FE1; EMBL: X15525; NID: g34239; PIDN
A; Cross-references: UNIPROT: P11117; UNIPARC: UP10000131FE1; EMBL: X15525; NID: g34239; PIDN
Bur. J. Biochem. 183, 611-616, 1989
A; Title: Structure of the human lysosomal acid phosphatase gene.
A; Reference number: $05525; MUID: 89377828; PMID: 2776754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1.423 <POH>
A;Cross-references: UNIPARC:UP10000131FE1; EMBL:X12548; NID:g34262; PIDN:CAA31064.1; PID
A;Note: part of this sequence, including the amino end of the mature protein, was confit
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A;Residues: 1-29 <GBI>
A;Cross-treferences: UNIPARC:UPI00001727CD
R;Pohlmann, R.; Krentler, C.; Schmidt, B.; Schroeder, W.; Lorkowski, G.; Culley, J.; Mer
EMBO J. 7, 2343-2350, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Human lysosomal acid phosphatase: cloning, expression and chromosomal assignmer
A;Reference number: S01155; MUID:89052645; PMID:3191910
A;Accession: S01155
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                                                                                                                                                                                                           NiAlternate names: acid phosphatase, lysosomal C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 04-Dec-1992 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004 C; Accession: S06167; S05525; S01155 Sivon Figura, K. submitted to the EMBL Data Library, June 1989 A; Reference number: S06167
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QSARQLRNAEALTLKSPAQRVTLELKGCPV-DANGFCPLDKFDNVMNTA 411
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                                                                                                                                                                                    phosphatase (EC 3.1.3.2) ACP2 precursor [validated] - human
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23.1%; Pred. No. 0.0023;
ve 44; Mismatches 180; Indels
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Best Local Similarity 23.1%;
Matches 98; Conservative 4
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A;Gene: GDB:ACP2
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A; Molecule type: DNA
A; Residues: 1-386 <SHA>
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acid phosphatase (EC 3.1.3.2) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jun-1900 #sequence_revision 29-Jun-1990 #text_change 09-Jul-2004
C;Accession: A31395
R;Himeno, M.; Fujita, H.; Noguchi, Y.; Kono, A.; Kato, K.
Biochham. Biochham. 162, 1044-1053, 1389
A;Title: Isolation and sequencing of a cDNA clone encoding acid phosphatase in rat liver
A;Reference number: A33395; MulD:89350910; PMID:2764916
A;Reference number: A33395
A;Status: prelliminary
A;Molecule type: mRNA
A;Residues: 1-423 «HIN»
A;Residues: 1-423 «HIN»
A;Cross-references: UNIPROT:P20611; UNIPARC:UPI0000131FE2; GB:M27893; NID:g202933; PIDN:
C;Superfamily: mammalian acid phosphatase
C;Keywords: phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
C;Keywords: phosphohistidine intermediate) #status predicted
F;42/Active site: Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 PTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVD-ERTRKT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHRQTAFRELERVIAFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 LTEIFL------LQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF-YLLQRTPEVA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 RSR-----ATPLLDLIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 WILPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGGVKL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NGKQAPYASCHIFELYQ--EDNGNF-SVEMYFRNDSK----FAPW------PL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 LANLTLETIWAVYDTLFCEQTHGLLLPPW---ASPQTVQALSQLKDFSFLFLFGIHDQVQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAILIPFL--SLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AEANLAGLEPP----TEVQHFNPNISWQPI-----PVHTVPITE------
                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 131; DB 2; Length 423; 22.8%; Pred. No. 0.011; tive 49; Mismatches 184; Indels 122;
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Best Local Similarity
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A;Cross-references: UNIPARC:UP10000039832; GB:M97589; NID:g189611; PIDN:AAA60021.1; PID::
R;Van Etten, R.L.; Davidson, R.; Stevis, P.E.; MacArthur, H.; Moore, D.L.
A; Biol. Chem. 266, 2313-2319, 1991
A;Title: Covalent structure, disulfide bonding, and identification of reactive surface a
A;Reference number: A38608; MUID:91115848; PMID:1989985
A; Molecule type: mRNA
A; Residues: 1-386 < SH3>
                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-386 <VAN>
                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: S14742
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosiduse: 1-421 <GEI>A;Cross-references: UNIPROT:P24638; UNIPARC;UPI0000027103; EMBL:X57199; NID:g52870; PIDN
C;Superfamily: mammalian acid phosphatase
C;Keywords: lysosome; phosphoric monoester hydrolase
                                                                                                                                                                                                                                     09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                              phosphatase
                                                                                                                                            acid phosphatase (EC 3.1.3.2) precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
C;Accession: S14742
R;Geier, C.; von Figura, K.; Pohlmann, R.
Biol. Chem. Hoppe-Seyler 372, 301-304, 1991
A;Title: Molecular cloning of the mouse lysosomal acid phosphata
A;Reference number: S14742; MUID:91282986; PMID:2059337
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404
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                                                                                                                                                                                                                                                                                                                  116 RKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIA 175
                                                                                                                                                                                                                                                                                                                                                                                                                       176 DFTGHROTAFRELERVINFPOSNLCLKREKODESCSLTOALPSELKVSADNVSLTGAVSL 235
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                                                                                                                                      109 LMSAEANLAGLFPP-----NEVQHFSPNISWQPI-----PVHTVPITE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 ASMLTBIFL------LQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 ETGLÍNVILETIWNVYDTLFCEQTHGLLLPPWASPQTVQRLSQLKDFSFLFLFGIHEQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 KARLOGGVLLAQILKNLTLMATTSQF-----PKLLVYSAHDTTLVALQMALNVY----
                                                                                                     2 KAILIPF----LSLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPDINT PPGGELV FERWRRLSDINSOWI OVSLV POTLOOMRDKT PLSLNT PPGEVKLTLAGC
                                                      Indels 107;
  Length 421;
; Score 122.5; DB 2;
; Pred. No. 0.054;
49; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EERNAQGMCSLAGFTQIVNEARIP 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHR-----CPLODFLRL-TEPVIP 361
  5.3%;
                                                    97; Conservative
                           Similarity
Query Match
Best Local S
Matches 97
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NiAlternate names: acid phosphatase, prostatic; orthophosphoric monoester phosphohydrola Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: T.-Aug-1992 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
Cispecies: Ji Angel 1992 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
Cispecies: Ji Angel 1992
Aisharief, F.S.; Li, S.S.L.
Aisharief, F.S.; Li, S.S.L.
Aithle: Structure of human prostatic acid phosphatase gene.
Aiseference number: JH0610; MUID:92272747; PMID:1375464 acid phosphatase (EC 3.1.3.2) ACPP precursor [validated] - human

A;Cross-references: UNIPROT:P15309; UNIPARC:UPI0000039832; GB:M97580; GB:M97581; GB:M975 A;Accession: J80693

A;Cross-references: UNIPARC:UP10000039832; GB:M34840; NID:g189620; PIDN:AAA69694.1; PID: Notoce: part of this sequence, including the amino end of the mature protein, was confir. R;Vinko, P:; Virkkunen, P:; Henttu, P:; Roiko, K.; Solin, T.; Huhtala, M.L. FEBS Lett. 236, 275-281, 1988

A;Title: Molecular cloning and sequence analysis of cDNA encoding human prostatic acid A;Reference number: S01331; MUID:88312981; PMID:2842184

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A;Molecule type: mRNA A;Residues: 1-14,'A',16,'ASC',20,'CF',23,'C',25-65,'WIWPTHPA',74-211,'A',213-386 <VIH> A;Cross-references: UNIPARC:UP1000016A48C; EMBL:X52174; NID:g28321; PIDN:CAA36422.1; PID

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F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-386/Product: acid phosphatase ACPP #status experimental <MAT>
F;43,86/Active site: Arg #status predicted
F;44/Active site: His (phosphohistidine intermediate) #status predicted
F;94/Active site: acidonydrate (Asn) (covalent) #status experimental
F;94,220,333/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;161-372,215-313,347-351/Disulfide bonds: #status experimental
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A; Status: preliminary; translation not shown
A; Status: preliminary; translation not shown
A; Status: preliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-14, 'AFASC', 20, 'CF', 23, 'C', 25-45, 'H', 47-65, 'RIWPTHPA', 74-138, 'E', 140-156, 'R
A; Cross-references: UNIPARC: UPI000016AF1A; EMBL.X53605; NID:g35683; PIDN: CAA37673.1; PID
R; Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W
Submitted to the EMBL Data Library, April 1993
A; Description: Characterization of the promoter of the human prostatic acid phosphatase
A; Reference number: S38863
A; Accession: S38863
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Akesiduse 1-40 - CABAN-
Akesiduse: 10 - CABAN-
Akesiduse: 10 - CABAN-
Akesiduse: 10 - CABAN-
Akesiduse: 10 - CABAN-
Akesiduse: 1993
Akesiduse
A; Note: part of this sequence, including the amino end of the mature protein, was confir B; Sharief, F.S.; Lee, H.; Leuderman, M.M.; Lundwall, A.; Deaven, L.L.; Lee, C.; Li, S.S. Bacchem. Biophys. Res. Commun. 160, 79-86, 1989
A; Title: Human prostatic acid phosphatase: cDNA cloning, gene mapping and protein sequen A; Reference number: A32419; MUID:89228054; PMID:2712834
A; Rocession: A32419
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A;Cross-references: UNIPARC:UP10000039832; EMBL:U07097; NID:G515995; PIDN:AAB60640.1; PI
C;Gomment: This protein is synthesized under androgen regulation by epithelial cells of A;Gene: GDB:ACPP
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A;Introns: 40/3; 72/3; 101/3; 152/3; 185/3; 216/3; 260/3; 288/3; 323/2
C;Function:
A;Description: catalyzes the hydrolysis of a wide range of phosphate esters
C;Superfamily: mammalian acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
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A, Residues: 1-40 <BA2.
A, Crose-references: UNIDARC: UPI0000006BB; GB: X71391; NID: g416530; PIDN: CAA50514.1; PID:
A, Crose-references: UNIDARC: UPI0000006BB; GB: X71391; NID: g416530; PIDN: CAA50514.1; PID:
Biochem: Mol. Biol. Int. 33, 561-565, 1994
B, Title: NUCleotide sequence of human prostatic acid phosphatase ACPP gene.
A, Reference number: I37175; MUID: 95038536; PMID: 7951074
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A; Residues: 140 < VIRS
A; Cross-teferences: UNIPARC: UPI0000006BB; EMBL: X74961; NID: g439657; PIDN: CAA52913.1;
A; Lee, H.; Chu, T.M.; Li, S.S.L.; Lee, C.
B; Lee, H.; Chu, T.Y., 759-765, 1991
Biochem. J. 277, 759-765, 1991
A; Title: Homodimer and heterodimer subunits of human prostate acid phosphatase.
A; Reference number: S17042; MUID: 91336999; PMID: 1908222
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R; Banas, B.; Blaschke, D.; Fittler, F.; Hoerz, W.
Biochim. Biophys. Acta 1217, 188-194, 1994
A; Tittler, Analysis of the promoter of the human prostatic acid phosphatase gene.
A; Reference number: S42730; MUID:94153995; PMID:8110833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 EKSRLQGGVLVNEILNHM-----KRATQIPSYKKLIMYSAHDTTVSGLQMALDVYNGLL 307
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                                                                                                                                                                                  13 SISIGELFILIFFWIDRSVLAK----ELKFVTLVFRHGDRSPI-------DTFPTD
                                                                                                                                          3 AILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPT-
                                                                            Gaps
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Query Match 5.1%; Score 117; DB 1; Length 386; Best Local Similarity 19.8%; Pred. No. 0.13; Matches 87; Conservative 63; Mismatches 178; Indels 112;
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he: 28.7339 secs
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ORGANISM: Sus scrofa
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Sequence 34904, A
Sequence 34902, A
Sequence 56, Appl
Sequence 6294, Ap
Sequence 8296, Ap
Sequence 8296, Ap
Sequence 2758, Ap
Sequence 2758, Ap
Sequence 2564, Ap
Sequence 2564, Ap
Sequence 2564, Ap
Sequence 2123, Ap
Sequence 2123, Ap
Sequence 2123, Ap
Sequence 2123, Ap
Sequence 21359, Ap
                                                                                             (without alignments)
551.244 Million cell updates/sec
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1. / EMC Celerra SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

2. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

4. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

6. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. / EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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                                                                             June 13, 2006, 10:46:00 ; Search time 10.0917 Seconds
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Sequence
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-10-953-349-34904
US-10-953-349-34903
US-10-953-349-34903
US-10-953-349-34903
US-10-953-349-8296
US-10-953-349-8296
US-10-953-349-8296
US-11-293-697-2758
US-11-293-697-2258
US-11-293-697-3258
US-11-293-697-3258
US-10-953-349-22123
US-10-953-349-22123
US-10-953-349-2765
US-10-953-349-7
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Maximum Match 100%
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length: 2000000000
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35,	36,	37,	38,	39, A	40,	41,	42,	43,	44,	302	4496,	380	22620	221	1524,	152	32471	1522,	32470
Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence								
US-11-317-329-35	US-11-317-329-36	US-11-317-329-37	US-11-317-329-38	US-11-317-329-39	US-11-317-329-40	US-11-317-329-41	US-11-317-329-42	US-11-317-329-43	US-11-317-329-44	US-11-293-697-3024	US-10-471-571A-4496	US-10-953-349-38096	US-10-953-349-22620	US-10-953-349-22124	US-10-953-349-1524	US-10-953-349-1523	JS-10-953-349-32471	JS-10-953-349-1522	JS-10-953-349-32470
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78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78	77.5	77.5	77	77	77	77	77	77
56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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BESULT: 10.0-040-6

SEGUENCE 6, Application US/11270040

PUBLICATION US. US20060110762A1

SEQUENCE INVENTION: US20060110762A1

APPLICANT: Kapl., Jeong-Ki

TITLE OF INVENTION: SYNDROME VIRUS RECEPTOR COMPONENTS AND USES THEREOF

TITLE OF INVENTION: SYNDROME US. 10.70,040

FILING DATE: 2005-10.27

PRIOR FILING DATE: 2005-11.09

PRIOR FILING DATE: 2005-11.09

PRIOR FILING DATE: 2005-11.10

PRIOR FILING DATE: 2005-11.10

PRIOR FILING DATE: 2005-10.27

PRIOR FILING DATE: 2004-11.10

WHERE REALESD for Windows Vereion 4.0

SEQUENCE OF WARNER: PART CONSTRUCTION NUMBER: 05.21

PRIOR APPLICATION NUMBER: 06.22

PRIOR FILING DATE: 2004-11.10

WHERE PRESENTED TO NOS: 8

SECOND NOS: 8
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Sequence 34902, Application US/10953349

Sequence 34902, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICATION ALEXANDROV, NICKOLAİ et al.

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS.

CURRENT APPLICATION UMBER: US/10/953,349

CURRENT PILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PALENTIN VERSION 3.3

SEQ ID NO 34902

LENGTH: 472
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4.2%; Score 97; DB 6; Length 472;
Best Local Similarity 25.1%; Pred. No. 0.39;
Matches 81; Conservative 37; Mismatches 107; Indels 98;
                                                                                                                                                    ch 4.2%; Score 97; DB 6; Length 464; 11 Similarity 25.1%; Pred. No. 0.38; 81; Conservative 37; Mismatches 107; Indels
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                                                                                    , ORGANISM: Zea mays subsp. mays US-10-953-349-34903
SOFTWARE: Patentin version 3.3
SEQ ID NO 34903
LENGTH: 464
                                                                                                                                                                           Best Local Similarity
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDRON, Nickolai et al.
APPLICANT: ALEXANDRON, Nickolai et al.
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
CURRENT APPLICADINE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: BNCONDED THERBY
TITLE OF INVENTION: BNCONDED THERBY
FILE REPRESENCE: 2750-1579-1908.2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ THEREFORE PATENTIN VERSION 3.3
SEQ ID NO 34904
LENGTH: 460
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---ASPNALRVDMEEL 1604
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                                                                                      345 QPDNTP-----PGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEV 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 DCEASIDLPSDDLRPYLRVAYD-----AAPADKLSAI--LÓBPR--PERPDWVLIDYA 114
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25.1%; Pred. No. 0.38;
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                                                                                                                                                                           398 KLTLAG---CEERNAQGMCSLAGF 418
                                                                                                                                                                                                                                                                                                                      ; Sequence 34904, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
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US-10-953-349-34904
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Best Local Similarity 25.1:
Matches 81; Conservative
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US-10-953-349-34903
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3733 PEFRFDAGSGMATIRHPTPLALGHFHTVTLLRSLTQGSLIVGDLAPVNGTSQGKFQGLDL 3792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELERVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----OCFT------LDLKNVTCQWQQDHASSQGFFYHSRARCCPRDR-- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 NFPQSNLCLKREKQDESCSLTQALPSELKVSADNV-----SLTGAVSLASMLTEIFLLQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 -YPIWENCEBEEKTNPGLQTPQFSRCHFKSRNDSIIHILVEVTTAPGTVHSYLGSPFWIH 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 QAQGMPEPG--WGRITDSH---------QWNTLLSLHNAQF 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 QAVRLPTPNLHWREISSGHLELEWQHPSSWAAQETCYQLRYTGEGHQDWKVLEPPLGARG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 YLLORIPEVARSRATPLLDLIMAALIPHPP-----QKQAYGVTLPTSVLFIAG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PD------358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QLMQ-------WLTPRGGE-L
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1) Sequence 2424, Application US/10511937

2) Publication No. US20060088836A1

2) GENERAL INFORMATION:

3) APPLICANT: EXPRESSION DIAGNOSTICS, INC.

3) APPLICANT: Woodward, Robert

4) APPLICANT: Woodward, Robert

5) APPLICANT: Woodward, Robert

5) APPLICANT: Woodward, Robert

5) APPLICANT: Woodward, Robert

6) APPLICANT: Woodward, Robert

7) TITLE OF INVENTION: METHODS AND COMPOSITIONS

7) TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

7) FILE REFERENCE: 506612000104

7) CURRENT APPLICATION NUMBER: US/10/511,937

7) PRIOR PILING DATE: 2002-04-24

7) PRIOR PILING DATE: 2002-04-24

7) PRIOR FILING DATE: 2002-12-20

7) NUMBER OF SEQ ID NOS: 3117

7) SOFTWARE: PARCHITIN VEYBION 3.2

7) TANDER OF SEQ ID NOS: 3117

7) TOWARD OF SEQ ID NOS: 3117

7) TOWARD OF SEQ ID NOS: 3117
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                                                                                        3793 NEELYLGGYPDYGAIPKAGLSSGFIGCVRELRI 3825
                                                        398 --KLTLAGCEERNAQGMCSL-AGFTQIVNEARI
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CORGANISM: Homo sapiens
US-10-511-937-2424
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APPLICANT: Wanderbilt University
APPLICANT: Wanderbilt University
APPLICANT: Wanderbilt University
APPLICANT: Wallahan, Dennis E
APPLICANT: Washing E
APPLICANT: Ow. Shiming IN
TITLE OF INVENTION: IN VUO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
FILE REFERENCE: 1242/47/2/2 CIP
CURRENT PAPLICATION NUMBER: US/11/183,325
CURRENT FILING DATE: 2005-07-13-3
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR PILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 56
SOFTWARR: PatentIn version 3.3
SEQ ID NO 56
LENGTH: 4391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3436 EGGQLPP-----GH-----SVQDGVLRIQNLDQSCQGTYIC---QAHGPWGKAQAS 3478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3479 AQLVIQALPSVLINIRTSVQTVVVGHAVEFECLALGDPKPQVTWSKVGGHLRPGIVQ--- 3535
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  171 KPEDLTVVPDYVPPPTTVAHRGFEAREL--FKPGLVPDDSGVSEGHRFGVSIGESQIVGI 228
                                                                                     3625 MLMLPSVRPQDAGTYVCTATNRQGKVKAFAHLQVPERVVPYFTQTPYSFLPLPTIKDAYR 3684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 KLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G----LAPDCAITVHTQADT-----SSPDP-----LFNPLKTGVCQLDN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 ANVIDALLSRAGGSIADFIGHRQTAFRELERVINFPOSNLCLKREKQDESCSLIGAL--- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PSELKVSADNVSLIGAVSLASMLTEIFLLQQAQGMPEP--GWGRI-----TDSHQWNT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 LLSL----HNAQFYLLQRTPEVAR-----SRATPLLDLIMAALTPHPPQKQAY- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 GELVFERWRRLSDNSQWIQVSL-VPQTLQQMRDKTPLSL-----NTPPGEV---- 397
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                                                 360 WRRLSDNSQWIQVSLVPQTLQQMRDK--TPLSLNTPPGEVKLTLAGCE-----ERNAQG
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4.1%; Score 93.5; DB 7; Length 4391;
Best Local Similarity 21.4%; Pred. No. 21;
Matches 110; Conservative 50; Mismatches 186; Indels 167;
                                                                                                                                                                                281 SVVYAAFG---SEAKUTSAQLQT 300
                                                                                                                                              412 MCSLAGFTQIVNEARIPACSLRS 434
                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/11183325 Publication No. US20060104898A1 GENERAL INFORMATION:
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DATABASE ACCESSION NUMBER: P98160
DATABASE ENTRY DATE: 2003-02-28
RELEVANT RESIDUES: (1)..(4391)
US-11-183-325-56
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Sequence 8295, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILL REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILLING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN version 3.3
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                                                       372 SGSPNGLLSDIK-----PKNANLTFRRWSNYSAGLVDYRPGCQGLVNHRATSGIIMEHVN 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 GFRVENVDLK-WSDDDDVNAAMNVPLEFRPSTVNNVSFVGFTS--GLYTKLFESDYVMSL 483
                       140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADF-----TGHRQTAFRELERVL 192
                                                                                                                          NFPQSNLCLKREKQDESCSLTQALPSELKVS-ADNVSLTGAVSLASMLTEIFLLQQAQGM 251
                                                                                                                                                                    426 GFRVENVDLK-WSDDDDVNAAWNVPLEFRPSTVNNVSFVGFTS--GLYTKLFESDYVMSL 482
                                                                                                                                                                                                                            252 PEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADF-----TGHRQTAFRELERVL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 PEPGWGRITDSHOWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             562
                                                                                                                                                                                                                                                                                                                              312 GVTLPTSVLPIAGHDTNLANLGGALBLNWTLPGQPDN------TPPGGELVFERW 360
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                                                                                                                                                                                                                                                                                                                                                                              511 -KTLRNRIHFRSGSTSTGPS-----RWATPCHEERPKGYFMNRTPPPPGQSRKWEDW 561
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4.0%; Score 91; DB 6; Length 614;
Best Local Similarity 20.9%; Pred. No. 2;
Matches 50; Conservative 31; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  **Section 10. 1220060105376A1

**Publication No. US20060105376A1

**GENERAL INFORMATION:

**APPLICANT: HELIX RESEARCH INSTITUTE

**TITLE OF INVENTION: Novel full length cDNA

**PILE REPERENCE: H1-A0106

**CURRENT APPLICATION NUMBER: US/11/293,697

**CURRENT FILING DATE: 2005-12-05

**PRIOR APPLICATION NUMBER: US/10/108,260

**PRIOR APPLICATION NUMBER: US/10/108,260

**PRIOR APPLICATION NUMBER: US/10/108,260

**PRIOR APPLICATION NUMBER: US/10/108,260

**NUMBER OF SEQ ID NOS: 5288

**SOFTWARE: PatentIn Ver. 2.1
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484 -----FTSNHQYIT------
                                                                                                                                                                                                                                                                               483 -----FTSNHQYIT----
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LENGTH: 614
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 TSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADF-----TGHRQTAFRELERVL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 NPPQSNLCLKREKQDESCSLTQALPSELKVS-ADNVSLTGAVSLASMLTEIFLLQQAQGM 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 PEPGWGRITDSHQWNTLLSLHNAQPYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAY 311
                                                  ---KLTLAGCEER 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 GVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDN------TPPGGELVFERW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KTLRNRIHFRSGSTSTGPS-----RWATPGHEERPKGYFMNRTPPPPGQSRKWEDW 406
----LSAVLGLLLLRWQFPAHYRRLRHALWPSLPDLHRVLGQYLRDTAALSPPKA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.0%; Score 91; DB 6; Length 458; Best Local Similarity 20.9%; Pred. No. 1.3; Matches 50; Conservative 31; Mismatches 92; Indels
                                               RWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEV--
                                                                                                                                                                                                                                                                                                                         ; Sequence 8297, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                  408 NAQGMCSLAGFTQIVNEARIP 428
                                                                                                                                                                                  611 AESGSCCT---THIANHSYLP 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8297
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; ORGANISM: Arabidopsis thaliana
US-10-953-349-8296
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Best Local Similarity 20.99
Matches 50; Conservative
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US-10-953-349-8297
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LENGTH: 613
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1094 -QVAQNVALYTG-----DPNL----GLEL------FEAAGDIFFDGAWER--- 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1065 KKE------KEAHAW-----LQAGKIYYILRQSE------LVDLYI----- 1093
                             ----PGWGRITDSHQWNTLLSLHNAQFYLLQRT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AF-----PLFNPLKTGVCQLD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 NANV---TDAILSRAGGS-----POSN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 LC-LKREKQ-DESCSLT-QALPSELKVSADNVSLT-----GAVSLASMLTEIFL-LQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAQGMPERGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAALTPHPP 306
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                                                        773 LASLTPGTGQALRGP-LYTSLAQLYSHHGCHGPAITFMTQAVEASAIAGVRAIVDHLVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 GWLTPRGGELIAYLGHYQ--RQRLVA----DGLLAKKGCPQSGQVAIIADVDERTRKTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 LIPLIPOSAFAQSEPELKLESVVIVSRHGVRAP----TKATQLMQDVTPDAWPTWPVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Mismatches 163; Indels 144; Gaps
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Ly, Ngoc
APPLICANT: Morins, MacDonald
APPLICANT: Morins, MacDonald
APPLICANT: Morins, MacDonald
APPLICANT: MOSTINS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: MND MONITORING TRANSPLANT REJECTION
FILE OF INVENTION: MNDER: US/10/511,937
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT APPLICATION NUMBER: PT/US2003/012946
PRIOR PILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 86; DB 6; Length 1336;
21.4%; Pred. No. 17;
                                                                                                                                                                460 -EVTRPTATSKYDHPLGFMVTHVTEMQ 485
                                                                                                                      PEVARSRATPLLDLIMAALTPHPPQKQ
                                                                                                                                                                                                                                                                                     Sequence 2564, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
                           236 ASMLTEIFLLQQAQGMPE-
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SOFTWARE: Patentin version
SEQ ID NO 2564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           69 LLPELPTQISSSRPTRPRRCKSSSRPHL-----ARGRRSPLKAAQ--ODRGLPAWG 117
                                                                                                                                                                                                                                                                                                        61 TWPVKLGWLTPRG--GELIAYLGHY-ORORLVADGLLAKK------GCPOSGQVAII 108
                                                                                                                                                                                                                                                                                                                                                                                                       109 ADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAGGSIADFIGHRQTAFRELERVINFPQSNICLKREKQDE----SCSLIQALPSELKVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKK------GCPQSGQVAIIADVDERTRK-----TGEAFAAGLAPDCAI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 SKOWPCSSMPAKOAPPSCVSEG----SVKGRTOKENLPOTNKLKSLSRLAGKGPD--- 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 SFEMBEVOSPERETGNPLDM-----TSGTVGARVDRANSCQSDSSGFLEEPLFPLDLQM 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 INFPQSNLCLK---REKQDESCSLTQALPSELK------VSADNVSLTGAVSL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 FSSLLSDVSILPNRAEEKAGGESVQRTSVSAAKEHRRRMGKLLRRASK-QNIRRDCNPEV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 TVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELE-RV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 FLSLL--IPLTPQSAFAQSEPE-LKLESVVIVSRHG-----VRAPTKATQLMQDVTPDA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Gaps
                                                                                                                                                                                                        5 LIPPLSLLI----PLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SESFKVKDEVFVPFTKPWDCGABLAATSINHKONHLSLSVEHOSLOACDDLLPYPPHGLL
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                                                                                                                 ch 3.9%; Score 90; DB 7; Length 384; I Similarity 24.2%; Pred. No. 1.2; 66; Conservative 24; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 ADNVSLTGAVSLASMLTRIFLLQQAQGMPEPGW 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 GSGAAMTGSWA-------APPRPAW 274
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Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR PILING DATE: 2005-12-05
PRIOR PLING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENT VEX. 2.1
SOFTWARE: PATENT VEX. 2.1
SOFTWARE: PATENT VEX. 2.1
                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2758
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US-11-293-697-3284
                                                                                                               Query Match
Best Local Similarity
Matches 66; Conserv
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US-11-293-697-3284
LENGTH: 384
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Best Local S:
Matches 84
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Query Match 3.6%; Score 84; DB 7; Best Local Similarity 19.9%; Pred. No. 11; Matches 68; Conservative 52; Mismatches 93
                                                                                                                                                                                                                                                                                                                                         Sequence 3258, Application US/11291697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR PELING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3258

LENGTH: 725
                                       295 DLIMAALTPHPPQKQAYGVTLPTSVL 320
                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                         RESULT 14
US-11-293-697-3258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | : : : : : : : | 1
141 PQALAT-----RALPCPAHVVFRYQAGREDEL/IITEGEWLEVIEEGDADEWVKARNQHG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 LASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 PDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDA----ILSRAGGS--IADFTGHR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 10/052586
PRIOR APPLICATION NUMBER: 10/052586
PRIOR PILING DATE: 2002-01-15
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06320
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063540
PRIOR PILING DATE: 1997-10-28
PRIOR PILING 
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                                                 :: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
366 NSQWIQVSLVFQTLQQMRDKT-PLSLNTPPGEVKLTLAGCEE 406
                                                                                                                                                                                                                                                                                                            Sequence 350, Application US/10196749 Publication No. US20060094864A1 GENERAL INFORMATION:
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Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang, Zemin
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ORGANISM: Homo Sapien
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US-10-953-349-22123
US-10-953-349-22123
Sequence 22123, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION: US20060107345A1
FILE REPERENCE: 2750-1579PUS2
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION VNMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22123
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GEAFAAGLAFDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 GHRQTAPRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 QH--TVNTELEKQIS------NEVDSE------DLKWSSEVKHICGEDQIEDK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 LTEIFLLQQAQGMPEPGWGRITD----SHQWNTLLSLHNAQFYLLQRTPEVARSRATPL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 IDLIMAALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGG 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 ELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGC-EERNAQGM 412
-----IRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPE-----LS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 CSL-----AGFTQI-----VNEARIPACSLRSHHHHHH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 KSIKLSSETESSFSSADISKADVSSSPTPSSDLPSHDMLHN 254
253
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US-10-953-349-22123

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18;
                                                                                                                                                                                                                               85 RQRLVADGLLAKKGCPQSGQVAIIADVDERT---RKTGEAFAAGLAPDCAITVHTQADTS 141
                                                                                                                                                           142 SPDPLFNPLKTGVCQLD-NANVTDALLSRAGGSIADFTGHRQTAFRELERVLNFPQSNLC 200
                                                                                                                                                                                                                                                                            201 LKREKODESCSLTQALPSELKVSADNVSL----TGAVSLASMLTEIFLLQQAQGMPEPGW 256
                                                                                                                                                                                                                                                                                                    150 -----DLSPASQQSVAGQASKSGNDVLLDLLSIGSPSVESSSSTVDILSSNSSNKAP-- 201
                                                                                                                                                                                                                                                                                                                                               257 GRITDSHQWNTLLSLANAQFYLLQRTPEVARSRATPLLDLIMAALTPHPPQKQAYGVTLP 316
                                                                                                                                                                                                                                                                                                                                                                        202 ---VSSLDGLSSLSLSTK-----TISNAAPMMDL-LDGFAPIPPTEN-NGPVYP 245
                                                                                                                                                                                                                                                                                                                                                                                                                 317 TSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                             246 SVTAPES-----SIRLTFNFSKQPGN--PQTTVIQATFMALSSNT---YTDFVF 290
                                                                                          34 VIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWLTPRGGE-----LIAYLGHY----Q
                                     Gaps
Query Match 3.6%; Score 82.5; DB 6; Length 360; Best Local Similarity 21.1%; Pred. No. 5.4; Matches 82; Conservative 53; Mismatches 155; Indels 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 QT----LQOMRDKTPLSLNTPPGEVKLT 400
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                                                                                                           June 13, 2006, 10:17:14; Search time 139.266 Seconds (without alignments)
GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                                                                        - protein search, using sw model
                Copyright
                                                                      OM protein
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Title:	144.539 Million cell updates/sec US-10-601-319-2
Perfect score:	2302
Sequence:	1 MKAILIPPLSLLIPLTPOSAIVNEARIPACSLRSHHHHHH 440

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2589679 seqs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Post-processing: Minimum DB Maximum DB

geneeqp19808:* geneeqp19908:* geneeqp20008:* geneeqp20018:* geneeqp20018:* geneeqp2003a8:* geneseqp2006s:* geneseqp2004s:* geneseqp2005s:* Genesed 8: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aab37892 Escherich Aae15806 Escherich Aae15806 Escherich Ada1946 E. coli B Ado50292 Escherich Aeb50302 Escherich Aeb50302 Kangaroo Aab3625 Lama2/APP Aab3625 ILS/APPA Aab3625 R15/APPA Aab36263 ILS/APPA Aab36263 R15/APPA Aab36263 ILS/APPA Aab36263 ILS/APPA Aab36263 ILS/APPA Aab36263 Escherich Ada19450 E. coli K Adu19427 Protein e Ad63745 Escherich Ad016129 Escherich SUMMARIES AEE75413 ADOS0304 ADOS0304 ADDS0302 AAB36251 AAB3625 AAB3625 AAB3625 AAB3625 AAB3626 ADC87745 ADL16129 ADO50298 AAB37892 AAE22836 AAE15806 ADA19446 ADO50292 98588 Length DB Query Match 1 99.1 99.1 97.1 97.1 23302 23302 23302 23302 22335 22335 22335 22335 22335 22335 22335 22335 22335 2235 2235 2235 2235 2235 2235 2235 Result

Aed50820 Escherich	Aee75419 E. coli B	Aef15220 Escherich	Aae02631 E. coli a	Adl16131 Shigella	Aae02634 E. coli a	Adl16130 Shigella	Aae02635 E. coli a	Aay94753 E. coli a	Abr42161 Escherich	Aae02632 E. coli a	Ad102198 AppA. 5/2	Abr42162 Escherich	Aay01513 An Escher	Adc87743 Modified	Aef15219 Escherich	Adw76361 Phytage A	Ado50300 Escherich	Aed50818 Escherich	Aee75421 E. coli B	Aae15808 Escherich	Adal9451 E. coli K
AED50820	AEE75419	AEF15220	AAE02631	ADL16131	AAE02634	ADL16130	AAB02635	AAY94753	ABR42161	AAE02632	ADL02198	ABR42162	AAY01513	ADC87743	AEF15219	ADW76361	ADO50300	AED50818	AEE75421	AAE15808	ADA19451
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432	432	432	432	432	432	432	432	432	432	432	432	432	423	436	432	431	432	432	432	430	430
97.1	97.1	97.0	6.96	6.96	96.6	96.6	96.6	96.5	96.5	96.0	95.5	95.4	95.3	95.0	94.8	94.3	94.3	94.3	94.3	93.0	93.0
2235	2235	2232	2230	2230	2224	2224	2223	2221	2221	2210	2198	2197	2194.5	2188	2182	2171.5	2171	2171	2171	2141	2141
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	4	43	44	45

ALIGNMENTS

Improving the nutritional value of phytate-containing foodstuffs, using phytase enzymes which catalyze the liberation of inorganic phosphate from Bscherichia coli B; phytase enzyme; anabolic; phytate digestion; nutrition. AAB37892 standard; protein; 440 AA. Escherichia coli B phytase enzyme. 25-MAY-2000; 2000WO-US014846 99US-00318528 (first entry) (DIVE-) DIVERSA CORP. Short JM, Kretz KA; WPI; 2001-112081/12. Escherichia colf. N-PSDB; AAC88885 WO200071728-A1. 25-MAY-1999; the phytates. 07-MAR-2001 30-NOV-2000 AAB37892; AAB37892

The present sequence is a phytase enzyme from Bscherichia coli B. The enzyme catalyses the liberation of inorganic phosphate from the phytate in phytate-containing foodstuffs and can thus be used to improve the nutritional value of phytate rich ingredients Claim 1; Fig 1; 147pp; English.

Sequence 440 AA;

Gaps ö Query Match 100.0%; Score 2302; DB 4; Length 440; Best Local Similarity 100.0%; Pred. No. 2.7e-223; Matches 440; Conservative 0; Mismatches 0; Indels 0.

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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New dietary aids comprising sustained release biocompatible compositions, comprise agent that assists in digestion, useful for delivering enzymes, therapeutics, medicine or agents to an organism.
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                                          RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
            MKAILIPFISLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                                                                                                                                                                         LTPHPPOKOAYGVTLPTSVLP1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                                                                                      LIPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALBLAWTLPGQPDNTPPGGBLVFBRW
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                                                                                      APAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
                                                                                                                                  RQTAFRELERVI.NFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
                                                                                                                                                                              EI FLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
MKAILIPFLSLLIPLTPQSAPAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dietary aid; biocompatible composition; therapeutic; digestive tract; foodstuff; digestion; phytase; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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N-PSDB; AAD36473.
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biocompatible composition is effective upon oral consumption and release in the digestive tract of a subject. The dietary aids are useful for delivering enzymes, therapeutics, medicine and agents to an organism. The use of enzymes and other agents in digestive aids of livestock or domesticated animals not only improves the animal's health and life expectancy but also assists in increasing the health of livestock or the production of foodstuffs from livestock. The present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; nutritional value; feed treatment process; therapy; thermal tolerance; growth performance; alcoholic drink; biopulping; non-alcoholic drink; biobleaching; B phytase.
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                                                                                                                                                       Length 440;
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                                                                                                                                                    Match 100.0%; Score 2302; DB 5; Local Similarity 100.0%; Pred. No. 2.7e-223; les 440; Conservative 0; Mismatches 0;
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                                                                                                                            Sequence 440 AA;
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(first entry)

20-NOV-2003

ADA19446;

E. coli B phytase.

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The patent discloses recombinant bacterial phytase from Escherichia colicity 2 appA phytase. The enzyme has phytase activity and improved thermal colorance when compared with wild-type phytase. It has improved protease stability at low ph. The recombinant phytase is useful for improving the cutritional value of phytate-containing foodstuffs and subsequently in the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are also used for generating recombinant digestive system life forms, for producting or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of enziromentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed.

The present sequence is B. coll B phytase protein
                                                                                                                                                                      New bacterial phytage for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
                                                       O' donoghue
                                                       Garrett JB,
                                                    Gray KA, Barton NR,
                                                                                                                                                                                                                                                                               Claim 1; Fig 1, 170pp; English.
(DIVE-) DIVERSA CORP.
                                                    Kretz KA,
                                                                                                    WPI; 2002-083108/11
                                                                                                                         N-PSDB; AAD25460
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                                                    Short JM,
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                                                                                                        121 AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
                                                                                                                                                                                                     RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
                                                                                            TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
                                                                                                                                          APAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
                                                                                                                                                                                       RQTAPRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
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 100.0%; Score 2302; DB 5; Length 440; 100.0%; Pred. No. 2.7e-223; ive 0; Mismatches 0; Indels 0;
                       Matches 440; Conservative
            Similarity
Query Match
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Claim 1; Fig 1; 62pp; English

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LIPHPPQKQAYGVTLPTSVLPIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
                                                        RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGPTQ 420
                                                                          RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKT.LAGCEERNAQGMCSLAGFTQ 420
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The invention relates to an isolated Escherichia coli polynucleotide encoding a phytase enzyme appearing as ADA19450 and having amino acids modification from W68E, Q84W, A95P, K97C, S168E, R180Y, N226C or Y277D.

Also included the E. coli appa gene ADA1949 (or an oligonucleotide derived from it) or its mutant sequence ADA19452, expression vectors, containing foodstuff by contacting the phytate-containing foodstuff with a pure phytase enzyme mutated phytase (where the phytase enzyme catalyzes containing foodstuff), a method to produce an animal feed containing a microbial phytase (comprising culturing the plant cell, plant part or containing the plant cells, plants or plant into a composition for animal (comprising the plant cells, plants or plant into a composition for animals (comprising the plant seeds, plant cells, plants or plants or an animal able to benefit from (colls, plant parts or plants in admixture with a phytase enzymes (congruising administering to the human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzymes comprising administering to the human or animal the plant seed, plant cells, plant parts or plants of a transgenic plant whose genome contain an expression system which expresses a mucleotide sequence congrain an expression system which expresses a mucleotide sequence comprising a phytase enzyme, a transgenic non-human organism whose genome comprising a betarologous nucleic acid sequence encoding a phytase activity. The phytate enzyme is useful for improving the animal feed and for enhancing digestion in humans and animals. The

ADA19446 standard; protein; 440 AA. ADA19446 ID ADA1 RESULT 4

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Phytase; enzyme; phytate; appA gene; animal feed; inorganic phosphate; digestion enhancement; transgenic; thermal tolerance; protease stability.
                                                                                                                                                                                                                                                                                                                    Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing
                                                                                                                                                                                                                                                                                Garrett JB;
                                                                                                                                                                                                                                                                                Barton NR,
                                                                                                        /note= "Encoded by CGN"
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             digestion in humans and animals.
                                                                                                                                                                                                                                                                                Gray KA,
                                                                                                                                                                    97US-00910798.
99US-00259214.
99US-00291931.
                                                                                                                                                       24-MAY-2001; 2001US-00866379
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25-MAY-2000; 2000US-00580515
                                                                                                                                                                                                                                                                                        O' Donoghue E, Mathur EJ;
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
O' DONOGHUE E
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                                                                                                                                                                                                                                                                                Kretz KA,
                                                                          Escherichia coli B.
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                                                                                                                                                                      13-AUG-1997;
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RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420
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  24-MAY-2001; 2001US-00866379.
                                    GRAY K A.
BARTON N R.
GARRETT J B.
O'DONOGHUE E
                                                                                                                           WPI; 2004-374952/35.
                                                                                               Kretz K,
                                                                            MATHER E J
                   SHORT J N
KRETZ K.
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Mather EJ;
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invented method improves thermal tolerance and protease stability. It also improves the feeding value of phytate rich ingredients. The present sequence represents E. coli B wild-type phytase.
                                                                                                          TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
                                                                                                                                                                                       ROTAFRELERVINFPOSNICLKREKODESCSLTOALPSELKVSADNVSLTGAVSLASMLT
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                                                                                                1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                            Gaps
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                                                         Length 440;
                                                                            0; Indels
                                                       100.0%; Score 2302; DB 6;
100.0%; Pred. No. 2.7e-223;
iive 0; Mismatches 0;
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Misc-difference 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli B phytase enzyme.
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; 99US-00259214.
; 99US-00291931.
; 200US-00318528.
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                                                                            Matches 440; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli; B.
                                                                   Best Local Similarity
                                       Sequence 440 AA;
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13-APR-1999;
25-MAY-1999;
25-MAY-2000;
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                                                         Query Match
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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expressing the nucleic acid in a yeast under conditions that allow expressing the nucleic acid in a yeast. The invention also relates to modified phytase enzyme in the yeast. The invention also relates to stability at low pit. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytate rich ingredients, and in diet of numerous animals including mammals, fowls and fishes, commercially significant mammals such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as suppy, zebrafish, molly, swordtall, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase incorporated in to the daetary aid is safe for animals. The present sequence is Escherichia coli B phytase enzyme.
                                                                                                                                                                                                                                        Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAXKGCPQSGQVAIIADVDERTRKTGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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O'donoghue E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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    Garrett JB,
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Barton NR,
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 2; 74pp; English.
    Gray KA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of the Escherichia coll B phytase. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, where the polypeptide is a modified sequence (AEST5421) derived from the Escherichia coll K-12 appa phytase (AEST5419). The modification of the enzyme, comprising a series of protein. The specification of the enzyme, comprising a series of protein. The specification also claims a pharmaceutical composition; a kit; an immobilized phytase; a fertilizer or soil additive; a liquid supplement for preventing muscle cramps; a hydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising nutrient englas, and a plant food additive, all comprising nutrient availability in an environment all sample by degrading environmental phytic acid. The novel enzyme is a dietary supplement useful for treating, preventing or reversing osteoporosis or
                                                                                                                                                            enzyme; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture; osteoporosis; osteopathic; food.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Formulation useful as dietary supplement for treating, preventing reversing osteoporosis and bone loss, and preventing muscle cramps comprises one or more polypeptides having phytase activity.
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                                                                                                                                                                                                                                        /note= "Encoded by CGN'
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                                                                                                                                                                                                                   Location/Qualifiers
                                                                         AEE75413 standard; protein; 440 AA
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, Zorner
                                                                                                                                        E. coli B phytase SEQ ID NO: 2.
421 IVNEARIPACSLRSHHHHHH
              421 IVNEARIPACSLRSHIHHHHH
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99US-00259214.
99US-0021931.
99US-00318528.
2000US-00580515.
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                                                                                                                    (first entry)
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Baum W, Robertson DE,
                                                                                                                                                                                                                                                                                                                                                                                                                         GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
BAUM W.
ROBERTSON D E
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                                                                                                                                                                                             Escherichia coli B.
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KRETZ K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZORNER P.
                                                                                                                                                                                                                           Misc-difference
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24-MAY-2001;
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13-APR-1999;
25-MAY-1999;
                                                                                                                    23-FEB-2006
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                                                                                             AEE75413;
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(KRET/)
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bone loss, and preventing muscle cramps. The liquid supplement is useful for preventing muscle cramps. The method is useful for reducing pollution and increasing nutrient availability in an environment or environmental sample by degrading environmental phytic acid, where the environment environment comprises a soil or a body of water. The immobilized phytase is useful in foodstuffs for improving the feeding value of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
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                                                                                                                                                                                                                                Length 440;
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                                                                                                                                                                                                                            Score 2302; DB 10;
Pred. No. 2.7e-223;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli W phytase 875PH2 mutant enzyme.
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                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 440; Conservative 0
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                                                                                                                                     phytate rich ingredients.
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                  Sequence 440 AA;
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241 EIFLLQQQQQMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA 300
                                                                                                                                   301 LIPHPPOKQAYGVILPTSVLFIAGHDTVLANLGGALELNWTLPGQPDVTPPGGELVFERW 360
                                                                                                                                                                                                              361 RRLSDNSQWIQVSLVPQTLQQQMRDKTPLSLMTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420
181 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240
                                                                                                               LTPHPPQKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kangaroo rat Escherichia coli phytase 872PH1 mutant enzyme.
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01-MAR-1999; 99US-00259214.
13-ARR-1999; 99US-00291931.
25-MAY-1999; 99US-00318528.
25-MAY-2000; 2000US-00580515.
24-MAY-2001; 2001US-00866379.
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KRETZ K.
GRAY K A.
BARTON N R.
GARRETT J B.
O'DONOGHUE B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-374952/35.
N-PSDB; ADO50301.
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(GARR/)
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(MATH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow expressing the nucleic acid in a yeast under conditions that allow expression of the enzyme which has improved thermal tolerance and protease conditied phytase enzyme enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme and fishes, commercially commercially such as plygs, godes, laboratory rodens, commercially significant mammals such as plygs, godes, laboratory rodens, commercially significant avian species such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially farmed fish such as guppy, zebrafish, molly, swordtail, commercially making and baking, in dietary aids for animals. The method provides easy manufacture of the active indietary aids for animals. The present sequence is Eacherichia coli W phytase mutant enzyme. Note: The present sequence is not shown in the specification but has been derived from
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99.1%; Pred. No. 2.9e-221;
ive 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page; 74pp; English.
                                                                                                                               13-AUG-1997; 97US-00910798.
01-WAR-1999; 99US-00258214.
13-APR-1999; 99US-00291831.
25-WAY-1999; 99US-0031B528.
25-WAY-2000; 2000US-00580315.
24-WAY-2001; 2001US-00866379.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gray KA,
                                                                                              20-JUN-2003; 2003US-00601319
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N-PSDB; ADO50291, ADO50303.
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(BART) BARTON N R.
(GARK) GARRETT J B.
(ODON/) O'DONOGHUE E.
(MATH/) MATHER E J.
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Best Local Similarity
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KRETZ K.
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                       JS2004091968-A1
                                                        13-MAY-2004
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Lama2/APPA plasmid translated sequence.

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The invention relates to a method for producing phytase that involves providing a nucleic acid encoding phytase derived from a bacteria, and expressing the nucleic acid in a yeast under conditions that allow cappression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease grability at low pit. The phytase enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme can be used in foodstuffs to improve the feeding value of phytase enzyme and fishes, commercially commercial including mammals, fowls and fishes, commercially significant mammals such as plugs, godes, laboratory rodense, commercially significant mammals such as plugs, godes, laboratory rodense, commercially farmed fish such as guppy, zebrafish, molly, swordtail, significant avian species such as chicken, ducks, doves, parrot, etc., in dough making and baking, in dietary aids for animals. The method provides easy manufacture of the active ingredient loaded biocompatible composition, higher yields and loading efficiency. The phytase composition, higher yields and loading efficiency. The present sequence is kangaroo rat Bscherichia coli phytase mutant enzyme. Note: The present sequence is not shown in the specification but has been constructed. The present sequence is not shown in the specification but has been constructed.
Producing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid
                                                                                                                            Disclosure; Page; 74pp; English
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Sequence 440 AA;

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                                                     1 MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATOLMODVTPDAWP
                                                                                                       TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
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99.0%; Score 2279; DB 8; Length 440; 99.1%; Pred. No. 5.7e-221; ive 0; Mismatches 4; Indel8
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             Best_Local Similarity 99.1
Matches 436; Conservative
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                          Transgenic animal; salivary protein; phytase; phosphorus; animal growth; environmental pollution; pig.
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Pred. No. 1.6e-216;
0; Mismatches 2;
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99.5%;
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Best Local Similarity 99.5
Matches 430; Conservative
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AAB36257 standard; protein; 432 AA

(revised)
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12-SEP-2003 20-FEB-2001 AAB36257;

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BIFLLQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300
 181 ROTAFRELERVLNFPOSNLCLKREKODESCSLTOALPSELKVSADNVSLTGAVSLASMLT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated
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99.5%; Pred. No. 1.6e-216;
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N-PSDB; AAC68299.
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Escherichia coli.
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             proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the E. coli APPA phytase coding sequence. (Upp on 12-SEP-2003 to standardise OS field)
 present invention provides transgenic animals which produce
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                                                                                                                                  The present invention provides transgenic animals which produce desired proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet being excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the B. coli APPA phytase coding sequence. (Updated on 12-SEP-2003 to standardise OS field)
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                                                              Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nucleic as sequence including a heterologous transgene construct encoding the protein.
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                  Phillips JP
                                                                                                                Disclosure; Fig 18; 152pp; English.
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Matches 430; Conservative
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GUELPH
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Matches 430; Conservative
environmental pollution;
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                                                                                                                                               WO200064247-A1
                                                 Mus musculus
Escherichia
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Pred. No. 1.6e-216;
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Best Local Similarity 99.5%; Pred. No. 1.6e
Matches 430; Conservative 0; Mismatches
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                                                                                                                                  R15/APPA plasmid translated sequence.
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                                     AAB36260 standard; protein; 432 AA.
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                                                                                          (revised)
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N-PSDB; AAC68297.
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Escherichia coli.
Chimeric.
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Qy 301 LTPHPPQKQAYGYTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360

Bb 301 LTPHPPQKQAYGYTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360

301 LTPHPPQKQAYGYTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360

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302 LTPHPPQKQAYGYTLPTSVLFIAGHDTNLANLGGALENNWTLPGGPDNTPPGGELVFERW 360

303 LTPHPPQKQAYGYTLQQWRDKTPLSLATPPGEVKLTLAGGEERNAQGMCSLAGFTQ 420

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RESULT 1 PPA_ECOLI ID PPA_ECOLI STANDARD; PRT; 432 AA.	01-APR-1988,	01-AUG-1991,	DT 07-MAK-2006, entry version 63.		GN Name=appA; OrderedLocusNames=b0980; OS Racherichia coli	 	~	KN [1] DD NICTEMPINE SECTEBACE (GENOMIC DAE) AND DECTETA SECTEBACE OF 22_20	RX MEDLINE=90368616; PubMed=2168385;	RT "The complete nucleotide sequence of the Escherichia coli gene appA	RT reveals significant homology between pH 2.5 acid phosphatase and	ימ	י כי	KN [2] RN VITOR EQUIPMENT CONTROL CONTROL CONTROL	RE NOCESCIIDS SEQUENCE (LAKES SCALE GENOMIC UNA).	K. SIEALNELZ / MULDOSS) RX MEDITURE 9742617: DihMed 9278603: DOT=10.1126/erience 277.5331.1453.		RA Riley M., Collado-Vides J., Glasher J.D., Rode C.K., Mayhew G.F.,				XL Science 277:1453-1474(1997).		RC STRAIN-K12 / W3110:		_				RA Sample C. Sect. 1., lagamit n., labemoro n., mada c., lamamoro 1., RA Vano M., Horinchi T.:			RL DNA Reg. 3:137-155(1996).			KX MEDLINES-17/1/16; FUDMEGE-3038201; DOL=10.1016/0300-9084(8/)90045-9; DA TANARI E Danchin B .	יים פלד"		RT of transcription mediated by cyclic AMP, ";	
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                                                 "A new oxygen-regulated operon in Escherichia coli comprises the genes for a putative third cytochrome oxidase and for pH 2.5 acid phosphatase (appA).";
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"Crystal structures of Escherichia coli phytase and its complex with phytate.";
Nat. Struct. Biol. 7:108-113(2000).
-!- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
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MEDIINE-923-56556; PubMed=8387749; DOI=10.1006/abbi.1993.1261;
Greiner R., Konietzny U., Jany K.-D.;
"Purification and characterization of two phytases from Escherichia
                                                                                                                                                                             CHARACTERIZATION.

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Golovan S., Wang G., Zhang J., Forsberg C.W.;

"Characterization and overproduction of the Escherichia coli appA encoded bifunctional enzyme that exhibits both phytase and acid
                                                                                                                                                                                                                                                                    "Overexpression, site-directed mutagenesis, and mechanism of Escherichia coli acid phosphatase."; J. Biol. Chem. 267:22830-22836(1992).
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MUTAGENESIS.
MEDLINE=93054596; PubMed=1429631;
Ostanin K., Harms E.H., Stevis P.E., Kuciel R., Zhou M.-M.,
                            MEDLINE-92049231; PubMed-1658595; DOI-10.1007/BF00267454;
Dassa J., Fsihi H., Marck C., Dion M., Kieffer-Bontemps M.,
Boquet P.L.;
                                                                                             Greiner R., Jany K.-D.; "Characterization of a phytase from Escherichia coli."; Biol. Chem. Hoppe-Seyler 372:664-665(1991).
                                                                                       CHARACTERIZATION, AND PROTEIN SEQUENCE OF 23-34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; MS8708; AAA72086.1; -; Genomic_DNA.

EMBL; U00096; AAC74065.1; -; Genomic_DNA.

EMBL; D90735; BAA35745.1; -; Genomic_DNA.

EMBL; X05471; CAA29031.1; -; Genomic_DNA.

EMBL; MS8708; -; NOT_ANNOTATED_CDS; Genomic_DNA.

EMBL; BS8731; ABA20286.1; -; Genomic_DNA.

PIR; BS8733; BS8733.
                                                                                                                                                                Arch. Biochem. Biophys. 303:107-113(1993).
              NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-17.
                                                                                                                                                                                                                  phosphatase activities.";
Can. J. Microbiol. 46:59-71(2000).
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1 IDKW; X-ray; A=23-432.

1 IDKN; X-ray; A=23-432.

1 IDKO; X-ray; A=23-432.

1 IDKO; X-ray; A=23-432.
Biochimie 69:215-221(1987).
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PDB;
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MQDVTPDAWPTWPVKL -> NAGCHPRRMANLAGKT (in Ref. 3).
EL -> DV (in Ref. 4).
D -> S (in Ref. 4). Periplasmic appA protein. /FIId=PRO 0000023947. Nucleophile. Proton donor.

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Chen Y., Zhu Z., Zhang Z., He J.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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HSSP; P07102; 1104.
SMR; OGG088; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc_phophtse.
PR00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS ACID_PHOSPHAT 1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNGNOWN_1.
                                                                         Score 2235; DB 2;
Pred. No. 7.6e-163;
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Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
Giang B., Hou Y., Yu J., Jin Q.;
"Genome dynamics and diversity of Shigella species, the etiologic
agents of bacillary dysentery."
Nucleic Acids Res. 33:6445-6458(2005).
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27-SEP-2005, sequence version 1.
27-SEP-2006, entry version 5.
Phosphoanhydride phosphorylase.
Name=appA; OrderedLocusNames=SSO_0987; ORFNames=SSO_0987;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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GO; GO:0003993; F:acid phosphatase actīvity; IEA.
InterPro; IPR000566; HisAc_phophtse.
Pfam; PF00328; Acid phosphat A; 1.
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Enterobacteriaceae; Escherichia.
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                                                      Length 432;
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MEDLINE=93054596; PubMed=1429631;
Ostanin K., Harms B.H., Stevis P.E., Kuciel R., Zhou M.-M., van Etten R.L.;
                                                                                                          2; Indels
5B355D76B7377737 CRC64;
                                                   Score 2231; DB 2;
Pred. No. 1.5e-162;
1; Mismatches 2;
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MEDLINE=90368616; PubMed=2168385;
Dassa J., Marck C., Boquet P.L.;
"The complete nucleotide sequence of reveals significant homology between
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J. Bacteriol. 172:5497-5500(1990)
47056 MW;
                                                 Query Match 96.9%;
Best Local Similarity 99.3%;
Matches 429; Conservative
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QBRKD6 ECOLI PRELIMINARY;
QBRKD6;
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Enterobacteriaceae; Escherichia.
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MEDLINE=93054596; PubMed=1429631;
Ostanin K., Harms E.H., Stevis P.E., Kuciel R., Zhou M.-M.,
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                                                                                                                                                                                                                             432 AA; 46972 MW; AF86C41EA6193AC5 CRC64;
SMR; QBRKD6; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfan; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                 Match 96.8%; Score 2229; DB 2; Local Similarity 99.3%; Pred. No. 2.2e-162; Les 429; Conservative 0; Mismatches 3;
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07-FEB-2006, entry version 13.
Periplasmic phosphoanhydride phosphohydrolase
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Dassa J., Marck C., Boquet P.L.;
"The complete nucleotide sequence of
"The complete nucleotide sequence or
reveals significant homology between
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QBRKDB;
OL-UN-2002, integrated into UniProtKB/TrEMBL.
OL-UN-2002, sequence version 1.
OT-FEB-2006, entry version 13.
Periplasmic phosphoanhydride phosphohydrolase.
Periplasmic phosphoanhydride phosphohydrolase.
Name-spph;
BECherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteria; Escherichia.
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GO; GO:0003993; F:acid phosphatase activity; GO; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOHydrolase.
SEQUENCE 432 AA; 46972 MW; 755D5E4B1AD91
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HSSP; P07102;
SMR; Q8RKD7; 2
[1]
NUCLEOTIDE SEQUENCE.
MEDLINE=90368616; PubMed=2168385;
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J. Bacteriol. 172:5497-5500.
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HSSP; P07102; 1DKM.
SMR; QBRKDB; 23-432.
GO; GO:0003993; F:acid phosphatase activity;
GO; GO:0016787; F:hydrolase activity; IEA.
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G0; G0:0016787; F:hydrolase activity; IEA.
InterPro; IFR000560; HisAc_phsphrse.
Pfam; PF00328; Acid_phosphat A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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RESULT 9
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ID Q8RKD9_ECOLI
AC Q8RKD9;

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SEQUENCE
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PubMed=16275786; DOI=10.1093/nar/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,

Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.

Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,

Qlang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species, the etiologic agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphoanhydride phosphorylase.
Name-appA; OrderedLocusNames-SBO 2250;
Shigella boydii serotype 4 (strain Sb227).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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Q31YP3;
Q6-DEC-2005, integrated into 1
06-DEC-2005, sequence version
Q7-FEB-2006, entry version 4.
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GO; GO:0003993;
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432 AA; 47064 MW;
                  IVNEARIPACSL
                                                                 RRLSDNSQWIQVSLVFQTLQQWRDKTFLSLNTFPGGEVKLTLAGCEERNAQGMCSLAGFTQ
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                                                                                                       LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                    LTPHPPQKQAYGVTLPTSVLF1AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                          EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATFLLDLIMAA
                                                  RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB66815.1; -; Genomic DNA. F:acid phosphatase activity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 2.6e-162;
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HSSP; P07102; 1DKQ.
SMR; OBKND; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtee.
Pfam; PF00328; Acid_phosphat_A; I.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Overexpression, site-directed mutagenesis, Escherichia coli acid phosphatase."; J. Biol. Chem. 267:22830-22836(1992).
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van Etten R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93054596; PubMed=1429631; Ostanin K., Harms E.H., Stevis P.E.,
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J. Bacteriol. 172:5497-5500(1990).
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Escherichia coli
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01-JUN-2002, sequence version 1.
07-FEB-2006, entry version 13.
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                                                     RRLSDNSQWIQVSLVFQTLQQMRDKTFLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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IVNEARIPACSL 432
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Creative Commons Attribution-NoDerivs License
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MEDLINE=90368616; PubMed=2168385;

Dassa J., Marck C., Boquet P.L.;

"The complete nucleotide sequence of the reveals significant homology between phelicose-1-phosphatase.";

J. Bacteriol. 172:5497-5500(1990).
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GO; GO:0016787; F:hydrolase activity; I
InterPro; IFR000560; HisAc_phsphtse.
Pfam; PF00328; Acid_phosphat A; I.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1;
Hydrolase.
SEQUENCE 432 AA; 46991 MW; 951F393E
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HSSP; P07102; 1DKM.
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MEDLINE=93054596; PubMed=1429631;
OStanin K., Harms E.H., Stevis P.E.,
van Etten R.L.;
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Pred. No. 4.5e-162;
0; Mismatches 3;
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RESULT 11
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05-JUL-2005, sequence
07-FEB-2006, entry 'Phosphoanhydride pho
Name=appA; OrderedLy
Shigella flexneri.
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Q83RW2_SHIFL
Q83RW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003993; F:acid phosphatase activity; IEA. InterPro; IPR000560; HisAc phsphtse. Pfam; PP00328; Acid phosphat A; 2. PROSITE; PS00616; HIS ACID PHOSPHAT 1; UNKNOWN 1. PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1. Complete proteome.

SEQUENCE 432 AA; 47106 MW; 25093A53992B9C1RC CT
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Yu J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang J., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE005674; AAN42610.2; -; Genomic_DNA. SMR; Q83RW2; 23-432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA
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OrderedLocusNames=SF0982;
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Pred. No. 7.6e-162;
1; Mismatches 4;
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InterPro; IPR000550,
InterPro; IPR000550,
InterPro; IPR000550,
IPR00328; Acid_phosphat_A; 1.
Pfam; PP00328; Acid_phosphat_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
PROSITE; PS00778; 
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SMR; Q6RK08; 23-432.
G0; G0:0003993; F:acid phosphatase activity;
InterPro, IPR000560; HisAc_phsphtse.
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Lei X.G.;
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MEDLINE=99194564; PubMed=10092520;
Rodriquez E., Han Y., Lei X.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
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pred. No. 9.1e-162;
0; Mismatches 4;
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RESULT 13

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STRAIN=2457T / ATCC 700930 / Serotype 2a;

MEDLINE=2590274; PubMed=12704152;

DOI=10.1128/IAI.71.5.2775-2786.2003;

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Enterobacteriaceae; Shigella.
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SMR; Q8CW75; 33.442.

BioCyc; ECCL199310:C1121-MONOMER; -.

BioCyc; ECCL199310:C1121-MONOMER; -.

GO; GO:0003993; F:acid phosphatase activity; IEA.

InterPro; IPR000560; HisAc phsphtse.

Pfam; PP00328; Acid phosphat A; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.

Complete proteome.

SEQUENCE 446 AA; 48606 MW; F1308CD691DB9F49 CRC6
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21-PEB-2006, entry version 15.
Periplasmic appA protein.
Name-appA; ORFNames=c 1121;
Escherichia coli 06.
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STRALN=06:H1 / CPT073 / ATCC 700928 / UPEC;

MEDLINE=22388234; PubMed=12471157; DDI=10.1073/pnas.252529799;

MEDLINE=22388234; PubMed=12471157; DDI=10.1073/pnas.252529799;

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Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

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Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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                           TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE 120
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Pred. No. 3.9e-161;
3; Mismatches 4;
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STRAIN-0157:H7 / Sakai / RIMD 0509952 / BEEG.

MEDLINE-21156231; PubMed-211289796; DOI=10.1093)dnares/8.1.11;

MEDLINE-21156231; PubMed-211289796; DOI=10.1093)dnares/8.1.11;

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakkawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
                                                                                                                                                                 InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid_phosphat A; 1.
PROSITE; PS00616; HIS ACID_PHOSPHAT 1; 1.
PROSITE; PS00778; HIS ACID_PHOSPHAT 2; UNKNOWN 1.
SEQUENCE 434 AA; 47337 MW; P197DF7D1869F9C4 CRC64;
                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                      Score 2210; DB 2; Length 434; Pred. No. 6.4e-161; 0; Mismatches 5; Indels
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ABP51937	AAE02632	ABR82310	AAE37851	AED46570	AEC39116	AAE37854	AED46568	AAE37853	ADO50302	AAE02635	AEE75413	ADO50292	ADA19446	AAE15806	AAE22836	AAB37892	AAE02634	ADOS0304	ADL16131	AAE02631	AEF15220
Abp51937 Phytase p	Aae02632 E. coli a	Abr82310 Nov9X phy	Aae37851 Maize-opt	Aed46570 Nov9x phy	Aec39116 Maize 27	Aae37854 pNOV4058	Aed46568 Nov9x phy		Ado50302 Kangaroo	Aae02635 E. coli a	Aee75413 E. coli B	Ado50292 Escherich	Ada19446 E. coli B	Aae15806 Escherich	Aae22836 Escherich	Aab37892 Escherich	Aae02634 E. coli a		Adl16131 Shigella	Aae02631 E. coli a	Aef15220 Escherich

ALIGNMENTS

ADO50300; Escherichia coli K12 appA phytase mutant 819PH59. 29-JUL-2004 ADO50300 standard; protein; 432 (first entry) ₽

AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; enzyme; mutant; mutein.

Escherichia coli; K12. Synthetic.

RESULT 1
AD050300
ID AD050300
ID AD050300
XX AD05
AC AD05
XX A 13-AUG-1997; 01-MAR-1999; 13-APR-1999; 25-MAY-1999; 25-MAY-2000; 24-MAY-2001; /note= "Wild-type Misc-difference 226 Misc-difference 181 /note= "Wild-type Lys replaced with Cys" Misc-difference 168 /note= "Wild-type Ala replaced with Pro" 20-JUN-2003; 2003US-00601319. 13-MAY-2004. US2004091968-A1 Misc-difference Misc-difference 95 Misc-difference 84 Misc-difference 68 97US-00910798. 99US-00259214. 99US-00291931. 99US-00316528. 2000US-00580515. 2001US-00866379. /note= "Wild-type Asn replaced with Cys" 277 /note= "Wild-type Ser replaced with Glu" 'note= note= "Wild-type Gln replaced with Trp" note= "Wild-type Trp replaced with Glu" "Wild-type Tyr replaced with Asp" Arg replaced with Tyr"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goate, laboratory rodents, commercially CC significant avian species such as guppy, zebrafish, molly, swordtail, CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase enzyme mutant.
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Best Local
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(KRET/)
(GRAY/)
(BART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 10;
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Mather EJ;
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(ODON/)
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BARTON N R.

GARRETT J B.

O'DONOGHUE E.

MATHER E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432
                                          RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                 LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                                                                                                                           AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
                                                                                                                                         EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
                                                                                                                                                            EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
                                                                                                                                                                                                                  YQTAFRELERVILNFPQSNILCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
                                                                                                                                                                                                                                                       AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
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IVNEARIPACSL 432
                          RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                providing nucleic acid derived from bacteria phytase activity, and expressing nucleic acid
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Pred. No. 3.2e-219;
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Misc-difference 284
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WPI; 2005-733851/75.
N-PSDB; AED50817, AED50824.
                           Short
                                                           (SHOR/)
(KRET/)
(GRAY/)
(BART/)
                                                                                                     25-MAY-2000;
24-MAY-2001;
                                                                                                                  13-APR-1999;
25-MAY-1999;
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                    Mathur
                                               (GARR/)
(ODON/)
                                                                                               24-MAY-2002;
                                                                                                                                01-MAR-1999;
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                 . дм,
ВЈ;
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                                       SHORT J M.
KRETZ K.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
MATHUR E J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
                          Kretz K,
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                                                                                                   99US-00318528.
2000US-00580515.
2001US-00866379.
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                                                                                               2002US-00156660
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                                                                                                                               97US-00910798.
99US-00259214.
                                                                                                                          99US-00291931.
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277
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357
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351
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226
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97
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RESULT 3
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Best Local S
Matches 432
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                                      Escherichia
                                                                                                                                  enzyme; mutein; thermostable; phytase; protein stabilization; pharmaceutical; fertilizer; cramp; cell culture; osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                             AEE75421
                                                                                                      osteopathic;
                                                                                                                                                                                                                                                                                                           23-FEB-2006
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                                                                                                                                                                                                                                        modified appA phytase
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                                                                                                      food;
                                                                                                                                                                                                                                                                                                       (first
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                                                                                                      appA
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Pred. No. 3.2e-219;
                                                                                                                                                                                                                                        819PH59
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The present sequence is that a novel modified phytase derived from the CC Escherichia coli appA protein, with improved thermal tolerance and CC protease stability compared to the wild-type. The present invention CC relates to a novel formulation, comprising at least one polypeptide CC (AEE7542) derived from the Escherichia coli K-12 appA phytase CC (AEE7542). The modification of the enzyme, comprising a series of CC (MEE7542). The modification of the enzyme, comprising a series of CC (MEE75419). The modification of the enzyme, comprising a series of CC mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition; a CC kit; an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising CC the novel phytase, and a method of reducing pollution and increasing CC nutrient availability in an environment or environmental sample by CC degrading environmental phytic acid. The novel enzyme is a dietary complement useful for treating, preventing or reversing osteoporosis or bone loss, and preventing muscle cramps. The liquid supplement is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1997;
01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                               Claim 1; SEQ ID NO 10; 82pp; English.
                                                                                                                                                                                                                                  Formulation useful as dietary supplement for treating, preventing or
reversing osteoporosis and bone loss, and preventing muscle cramps,
comprises one or more polypeptides having phytase activity.
                                                                                                                                                                                                                                                                                     WPI; 2006-055022/06.
N-PSDB; AEE75420.
                                                                                                                                                                                                                                                                                                                       Baum
                                                                                                                                                                                                                                                                                                                                                                                                                (SHOR/)
(KRET/)
(GRAY/)
(BART/)
                                                                                                                                                                                                                                                                                                                                   Short
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOGHUE E.
                                                                                                                                                                                                                                                                                                                                                         BAUM W.
ROBERTSON D
ZORNER P.
                                                                                                                                                                                                                                                                                                                  Kretz KA, G
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99US-00259214.

99US-0021931.

99US-00318528.

2000US-00580515.

2001US-00866379.
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Zorner
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Best Local S
Matches 432
  13-AUG-1997;
01-MAR-1999;
13-APR-1999;
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                                                                                                    24-MAY-2002;
                                                                                                                                                                                                         US2003103958-A1
                                                                                                                                                                                                                                                         Synthetic.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                   thermotolerance; thermostability; kernel; phytate; myo-inositol-hexaphosphate; inositol; inorganic phosphate, thermotolerant; feed value; digestion; enzyme.
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99US-00259214.
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Pred. No. 3.2e-219;
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                                                                                                                                                                                                                                                                                                                                                           The invention discloses a new isolated or recombinant nucleic acid which ce encodes a polypeptide having a phytase activity. Also claimed is a compose of the nucleic acid, a vector comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic composition of a phytase message in a cell, a heterodimer comprising the translation of caid, a hybridoma comprising immobilised polypeptide or nucleic acid, a hybridoma comprising an antibody that specifically binds to the colypeptide, a food supplement for an animal, an edible enzyme delivery carrier, an edible pellet comprising a granule edible carrier and the colypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, making an anti-phytase antibody, producing a recombinant colypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, contifying a modulator, whole cell engineering of new or modified composition and processing of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a digestive system and processing of corn and sorghum kernels. The phytase activity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or cash and in phytate digestion. The sequence presented is the modified
                                                                                                                                                                                                                                                                                       Matches 432;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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25-MAY-2000;
24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                           Sequence
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improving the feeding value of phytate rich
phytate digestion.
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DB; ADC87742.
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AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
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Pred. No. 3.3e-219;
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The patent discloses recombinant bacterial phytase from Escherichia coli Kl2 appA phytase. The enzyme has phytase activity and improved thermal tolerance when compared with wild-type phytase. It has improved protease stability at low pH. The recombinant phytase is useful for improving the nutritional value of phytate-containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are
                                                                                                                                                                                                                                        New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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Matches 430; Conserv
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                             Misc-difference
                                                                                Misc-difference
                                                                                                                                                                                                      Synthetic.
Escherichia coli; strain K12.
                                                                                                                                                                                                                                                                                       mutant; mutein.
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"Wild-type Gln substituted
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Condification from W68E, 084W, A95P, K97C, S168E, R180Y, N226C or Y277D.
CC Also included the E. coli appA gene ADA19445 and having amino acids
CC derived from it) or its mutant sequence ADA1945.
CC containing foodstuff by contacting the phytate-containing foodstuff by contacting the phytase containing foodstuff by contacting the phytase in the phytate in the phytate containing foodstuff), a method to produce an animal feed containing a containing foodstuff), a method to produce an animal feed containing a comprising culturing the plant cell, plant part or plant under conditions where the nucleotide sequence is expressed and converting the plant cells, plants or plants or plant into a composition for animal feed composition for animal (comprising the plant seeds, plant cells, plant parts or plants in admixture with a phytate-containing comprising the plant seeds, plant cells, plant parts or plants in admixture with a phytate-containing comprising the plant seeds, plant cells, plant parts or plants or plants or animal scomprising the plant seeds, plant cells, plant parts or plants or plants or animal the plant seeds, plant cells, plant parts or plants or human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzymes comprising administering to the human or animal the plant seed, plant cells, plant parts or plants of a transgenic plant which is modified to comprising a heterologous nucleic acid sequence encoding a polypeptide comprising a heterologous nucleic acid sequence encoding a polypeptide nutritional value of phytate-containing foodstuff, in the production of animal feed and for enhancing digestion in humans and animals. The containing the sequence represents E. coli K12 mutant phytase.

CC sequence represents E. coli K12 mutant phytase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Short JM,
O' Donogh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 59; Fig 8; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-040002/03.
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(KRET/)
(GRAY/)
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25-MAY-1999;
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01-MAR-1999;
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(GARR/)
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) BARTON N R.
) GARRETT J B.
) O' DONOGHUB E.
) MATHUR E J.
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                                   Rattus sp.
Escherichia
                                                                      environmental
                                                                                 Transgenic
                                                                                                       R15/APPA plasmid translated sequence
                                                                                                                                                                  AAB36261;
                                                                                                                                                                                       AAB36261 standard; protein;
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Pred. No. 1.6e
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No. 1.6e-211;
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AAB36262 standard; protein; 432

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N-PSDB; AAC68298.
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Pred. No. 1.6e-211;
D; Mismatches 8;
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                       LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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                                        The present invention provides transgenic animals which produce desired proteins, in this case pigs which expresses phytase in the salivary gland. Low phytase production levels result in phytate in the diet being excreted and causing phosphorus contamination in water, as well as reducing the growth of animals. The invention provides a number of transgenes containing the E. coli APPA phytase coding sequence. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                   Transgenic animal; salivary protein; phytase; phosphorus; environmental pollution; pig.
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              02-NOV-2000
                                                           Chimeric.
                                                                     Rattus sp.
Escherichia
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20-FEB-2001
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98.1%;
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Pred. No. 1.6e-211;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic non-human animal for gastrointestinal tract specific expression of a protein, preferably phytase, comprises a nucleic acid sequence including a heterologous transgene construct encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 432 AA;
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milarity 98.1%;
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Pred. No. 1.6e-211;
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                    AAE15807 standard; protein; 432
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                                                                                                                RRLSDNSQWIQVSLVFQTLQQWRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                                            RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVXLTLAGCBERNAQGMCSLAGFTQ
                                                                                                                                                          LTPHPPQKQAYGVTLPTSVLF I AGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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98.1%;
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ed. No. 1.6e-211;
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                                                                                                                                                                                                                                                                                                                                                                 The patent discloses recombinant bacterial phytase from Escherichia coli CK K12 apph phytase. The enzyme has phytase activity and improved thermal CC tolerance when compared with wild-type phytase. It has improved protease stability at low pH. The recombinant phytase is useful for improving the mutritional value of phytate-containing foodstuffs and subsequently comproving the growth performance of an organism that consumes it, in treating animal digestive systems, in feed treatment processes and for in vitro purposes related to research, discovery and development. They are also used for generating recombinant digestive system life forms, for producing or manufacturing alcoholic and non-alcoholic drinks based on the use of moulds, grains and/or plants, in biopulping and bio-bleaching where a reduction in the use of environmentally harmful chemicals that are traditionally used in the pulp and paper industry is desired and in the reduction or possible elimination of the need for mineral supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed. The present sequence is E. coli apph phytase wild type protein
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Best Local S
Matches 424
                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial phytase; K12 appA phytase; protease stability; anabolic; gastrointestinal; nutritional value; feed treatment process; therap thermal tolerance; growth performance; alcoholic drink; biopulping; non-alcoholic drink; biobleaching.
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                                                                                                                                           TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
                                YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
                                                                                          AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
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Search Job tim	DЪ	Ş	В	Ş	В	Ş	В	Ş
Search completed: June 13, 2006, 10:22:05 Job time : 138.734 secs	421 IVNEARIPACSL 432	421 IVNEARIPACSL 432	361 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420	361 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420	301 LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360	301 LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360	241 EIFLLQQAQGMPEPGMGRITDSHQMNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTA 300	241 BIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA 300

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Result
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                    Score
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-866-379-2
US-09-866-379-2
US-09-866-379-2
US-09-868-379-2
US-09-89-135-1
US-09-489-039A-13501
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          Sequence 10, Appl
Sequence 8, Appli
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Sequence 120, Appli
Sequence 121, Appli
Sequence 121, Appli
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	Sequence 79	Sequence 80	Sequence 80	Sequence 8,	Sequence 153,	Sequence 130	Sequence 108	Sequence 33,	Sequence 165	Sequence 7,	Sequence 152	Sequence 129	Sequence 107	Sequence 6,	Sequence 78	Sequence 33	Sequence 8,	sequence a,
, Appl	, Appl	, Appl	, Appl	×		0, App			5, App	Appli	2, App	9, App	7, App	~	•	•		TIGGA

ALIGNMENTS

APPLICANT: BARTON, No. 1. APPLICANT: GARRETT, James APPLICANT: O'DONOGHUE, Eileen FITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND FILE REFERENCE: DIVER1370-7 CURRENT APPLICATION NUMBER: US/09/866,379 CURRENT FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 09/580,515 PRIOR FILING DATE: 2000-05-25 PRIOR FILING DATE: 1999-05-25 PRIOR FILING DATE: 1999-05-25 PRIOR APPLICATION NUMBER: US 09/291,931 PRIOR APPLICATION NUMBER: US 09/297,931 ; ORGANISM: Artificial Sequence ; PEATURE: OTHER INFORMATION: Modified phytase US-09-866-379-10 ; Sequence 10, Application US/09866; Patent No. 685365; GENERAL INFORMATION: ; APPLICANT: DIVERSA CORPORATION APPLICANT: SHORT, Jay ; APPLICANT: KETZ, Keith APPLICANT: GRAY, Kevin US-09-866-379-10 Query Match Best Local Similarity Matches 430; Conserva SOPTWARE: PatentIn version 3.1 SEQ ID NO 10 LENGTH: 430 TYPB: PRT Application US/09866379 98.7%; Score 2228; DB 2; 99.5%; Pred. No. 2.3e-227; tive 0; Mismatches 0; Length 430; AND USES THEREOF

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AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH 180

430;

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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR PRIOR DATE: 1099-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR PRILING DATE: 1999-03-01
PRIOR PRILING DATE: 1999-03-01
PRIOR PRILING DATE: 1999-03-01
PRIOR PRILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GO'DONGHUE, Eileen
TITLE OF INVENTION: RECOMBIANT BACTERIAL PHYTASES AND FILE REFERENCE: DIVER1370-7
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                                                                                                                                                       Matches
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AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
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98.1%;
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; ORGANISM: Escherichia
US-09-715-477-1
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Best Local Similarity
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GENERAL INFORMATION:

APPLICANT: Le1, Xingen
ITILE OF INVENTION: SITE-DIRECTED MUTAGENES
FILE REFERENCE: 19603/4031
CURRENT FILING DATE: 2000-11-17
CURRENT FILING DATE: 2000-611-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 432
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ilarity 97.9%;
Conservative
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GENERAL INFORMATION:
APPLICANT: Kretz, Keith
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVER1370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                            RESULT 5
US-09-318-528-2
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GENERAL INFORMATION:
APPLICANT: K-etz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
                                                                               Sequence 2, Application Patent No. 6183740
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Best Local Similarity
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TYPE: PRT
ORGANISM: Escherichia coli
0-09-259-214-2
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Pred. No. 2.7e-221;
0; Mismatches 10;
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; TYPE: PRT ; ORGANISM: Escherichia US-09-291-931-2

LENGTH:

440

NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows SEQ ID NO 2

Version

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GENERAL INFORMATION:

APPLICANT: Kretz, Keith
ITITLE OF INVENTION: MOVEL PHYTASE
FILE REFERENCE: 09010/029003

CURRENT APPLICATION NUMBER: US/09/291,931A

CURRENT FILING DATE: 1999-04-13

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER FILING DATE: 1997-08-13

EARLIER APPLICATION NUMBER: 09/259,214

EARLIER APPLICATION NUMBER: 09/259,214
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EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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US-09-291-931-2
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                                                                                                                                                                   Sequence 2, Applic Patent No. 6190897
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Best Local Similarity
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ORGANISM: Escherichia
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                                                                                                                                                                                     Application
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Pred. No. 2.7e-221;
0; Mismatches 10;
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                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Escherichia US-09-580-515-2
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/580,515
CURRENT FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 08/910,798
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1997-08-13
PRIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
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US-09-580-515-2
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Patent No. 6720014
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2
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Best Local Similarity
                                                                                                                                   Matches 422;
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Best Local Similarity
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TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
                                                           MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                           MKAILIPFLSLLIPLTEQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP 60
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Pred. No. 2.7e-221;
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Pred. No. 2.7e-221;
0; Mismatches 10; Indels
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APPLICANT: GARRY, Revin
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
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; TYPE: PRT
; ORGANISM: Escherichia
US-09-866-379-2
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US-09-866-379-2
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Nelson
APPLICANT: GRARETT, James
                                                                                                                                                                Query Match
Best Local Similarity 97.7
Matches 422; Conservative
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Patent No. 6855365
                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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Pred. No. 2.7e-221;
0; Mismatches 10;
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Sequence 3, Application US/09715477

Patent No. 6841370

GENERAL INFORMATION:
APPLICANT: Lei, Xingen
ITILE OF INVENTION: SITS-DIRECTED MUTAGENESIS OF FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/09/715,477
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR APPLICATION NUMBER: 60/166,179
PRIOR PILING DATE: 1999-11-18
NUMBER OF SEO ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 432
TYPE: PRT
ORGANISM: Escherichia coli
US-09-715-477-3
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                                                             EIFLLQQAQGMPBPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
                                                                                                  ROTAFRELERVLNFPQSNLNLKREKQNESCNLTQALPSELKVSADNVSLTGAVSLASMLT
                                                                                                               YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
                                                                                                                                                   AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
                                                                                                                                                                   AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH
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RESULT 11 US-09-540-149A-1

Sequence 1, Application US/09540149A Patent No. 6511699
GENERAL INFORMATION:

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APPLICANT: Le1, Xingen
ITILE OF INVENTION: PHOSPHATASESS WITH IMPROVED PHY
FILE REFERENCE: 19603/2798
CURRENT APPLICATION NUMBER: US/10/266,041A
CURRENT ETLING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
PRIOR PILING DATE: 1999-03-31
PRIOR PILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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TYPE: PRT
ORGANISM: Escherichia
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                IVNEARIPACSL 432
                                                                 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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IVNEARIPACSI 432
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Pred. No. 9.3e-219;
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; LOCATION: (433)
; OTHER INFORMATION: Xaa at position 433 in this sequence is unknown
US-09-540-149A-1
                                                                                                                                                                                                                                                              RESULT 12
US-08-910-798-2
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TITLE OF INVENTION: SZYMES WITH IMPROVED PHYTASE .
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR PILING DATE: 1999-03-31
NUMBER OF SEG ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                         Sequence 2, Application Patent No. 5876997 GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
                                                                                                                                       TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                              APPLICANT: KRETZ
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                                                                   CITY: La Jolla
STATE: California
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Pred. No. 9.3e-219;
0; Mismatches 14;
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                                                                                                                                                                                                                    RESULT 13
US-09-489-039A-7512
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                                                                                                                                                             Sequence 7512, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION UNMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619,678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,798
FILLING DATE: AUGUST 13,1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TOPOLOGY: linear

LECHT TOPOLOGY: linear
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Pred. No. 6.5e-210;
0; Mismatches 10;
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US-09-489-039A-13501
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7512
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                                                                                                                                                                                                                                                 Query Match 16.9
Best Local Similarity 26.3
Matches 117, Conservative
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LENGTH: 522
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Patent No. 6610836
GENPDAY ....
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
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Best Local Similarity
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EAFAAGLAFDCAITVHTQADTSSFDFLFNFLKTGVCQLDNANVTDAILERAGGSIADFTG 179
                                                                                                                                                            GULRUFIACALPULALQSAAA---ADWQLEKVVELSRHGIRPPTAGNREAIEAATGRPW
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                                                                                                                 PTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTG
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                                                                                                                                                                                                                                                 16.9%; Score 381; DB 2; Length 522, 26.3%; Pred. No. 3.3e-31; ative 73; Mismatches 209; Indels
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32.6%; Pred. No. 1.5e-48;
ative 70; Mismatches 181;
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TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3
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SOFTWARE: PatentIn Ver.
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 102;
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: WYSS, MARKUS
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044, 718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 5.6%; Score 126; DB 2; Length 439; Local Similarity 20.9%; Pred. No. 0.00028; es 102; Conservative 69; Mismatches 166; Indels 150;
                                                                                       214 QALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 PFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPT----KATQLMQDVTPDA---
                                                                                                                                                                                                                                                                                                                                                   -----WPTWPVKLG--ELTPRGGELIAYLG--HYWRQRLVADGLLPKCGCPQSGQVAII 108
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PASAMONTES, Luis
TOMSCHY, Andrea
van LCON, Adolphus
VOGEL, Kurt
                                               -- LPGVTLTDEDVVSLMDMCSFDTV----
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                                                                                                                                       CTKFEASQLGDEV-----AANFTALFAPDIR-----ARAEKH-----
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TPE-VARSRATPLLDLIKT--ALTPHP 305
                                               -ARTSDASQLSPFCQLFT 258
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Gaps

Sear	Db	Ş	밁	Ş	B	Ş	В
Search completed: June 13, 2006, 10:30:46 Job time : 36.6697 secs	423 KGLSWAR 429	420 QIVNEAR 426	365 DGYSASWVVPFGARAYFETMQCKSEKEPL-VRALINDRVVPLHGCDV-DKLGRCKLNDFV 422	364 SD-NSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFT 419	319ATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVESAKEL 364	306 PQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRL 363	::: : :

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Match
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Listing first 45 summaries
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US-11-505-928-150
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Sequence 3, Appli
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Sequence 33870, A	Sequence 33871, A	Sequence 4496, Ap	Sequence 50, Appl	Sequence 22620, A	Sequence 3258, Ap	Sequence 284, App	Sequence 6, Appli	Sequence 300, App	•	Sequence 11734, A		Sequence 32470, A	Sequence 32471, A	Sequence 34902, A	34903,	Sequence 34904, A	Sequence 11735, A	Sequence 56, Appl	Sequence 46, Appl

ALIGNMENTS

APPLICANT: Frentato, MacDonald APPLICANT: ROSENDERG, Steven ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING ITITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING ITITLE OF INVENTION: METHODS AND MONITORING TRANSPLANT REJECTION PLIC REFERENCE: 506612000104 CURRENT APPLICATION NUMBER: US/10/511,937 CURRENT FILING DATE: 2004-10-19 PRIOR APPLICATION NUMBER: PCT/US2003/012946 PRIOR APPLICATION NUMBER: US 10/131,831 PRIOR APPLICATION NUMBER: US 10/131,831 PRIOR APPLICATION NUMBER: US 10/325,899 PRIOR PILING DATE: 2002-04-24 PRIOR APPLICATION NUMBER: US 10/325,899 PRIOR PILING DATE: 2002-12-20 NUMBER OF SEQ ID NOS: 3117 SOPTWARE: PatentIn version 3.2 SEQ ID NO 2424 LENGTH: 635 Sequence 2424, Application US/10511937 Publication No. US20060088836A1 GENERAL INFORMATION: APPLICANT: EXPRESSION DIAGNOSTICS, INC. APPLICANT: Wohlgemuth, Jay APPLICANT: Wohlgemuth, Jay APPLICANT: Woodward, Robert APPLICANT: Ly, Ngoc APPLICANT: Ly, Ngoc APPLICANT: Prentice, James APPLICANT: Prentice, James ş ફ 밁 밁 Ś ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-511-937-2424 RESULT 1 US-10-511-937-2424 Query Match 4.5%; Score 101.5; DB 6; Length 635; Best Local Similarity 20.4%; Pred. No. 0.23; Matches 115; Conservative 60; Mismatches 195; Indels 193; 243 183 TVIQLIATETCCPALQRPHSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGSCL 123 RVLFVDSVGLPAPPSIIKAMGGŚQPGELQISWEEPAPEIŚDFLRYELRYGPRDPKNSTGP 182 77 IAYL---GHYWRQ-RLVADGLLPKCGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAI 132 49 ---QLMQ-------ELTPRGGE-L 2 KAILIPFLSLLIPLTPQSAFAQSEP-ELKL---ESVVIVS-----RHGVRAPTKAT--ISGLOPGNSYWLOLRSEPDG-ISLGGSWGSWSLPVTVDL-----PGDAVALGL-----Gaps

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US-11-293-697-2758
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2758, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
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Best Local
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 384
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  APPLICANT: Numez, Gabriel
APPLICANT: Numez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular:
FILE REFERENCE: UM-06967
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEG ID NOS: 44
SOFTWARE: Patentin version 3.1
SEG ID NO 34
LENGTH: 765
TWORD: DET
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Publication No. US20060105413A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/11317329 Publication No. US20060105413A1
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TITLE OP INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
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TYPE: PRT
ORGANISM: Homo sapiens
TYPB: PRI
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Pred. No. 1.6;
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US-11-317-329-35
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SEQ ID NO 35
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/11317329 Publication No. US20060105413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                Query Match 4.1%; Score 93.5; DB 7; Length 765; Best Local Similarity 21.6%; Pred. No. 1.6; Matches 88; Conservative 46; Mismatches 144; Indels 129;
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Best Local Similarity
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APPLICANT: Inchara, Nachiro
TITLE OPT INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR PILICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
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CQT-----ASGYTPLLIAAQDQQPDLCALLLAHGADANRVDEDGWAPLHFAAQNGDDR
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US-11-317-329-36
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOPTWARE: Patentin version 3.1
SEQ ID NO 3.6
SEQ ID NO 3.6
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Publication No. US20060105413A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
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ORGANISM: Homo
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                                         ----VTLPT----SVLFIAGHDTNL-----ANLGGALELNWT 341
YGASLELPTHQGWTPLHLAAYKGHLEIIHLLAESHANMGALGAVNWT
                                                                                                                                                                                                                                                                TARLLIDHGACVDA-QEREGWTPLHLAA--QNNFENVARLLVSRQADPNLRE-----
                                                                                                                                                                                                                                                                                                         ----LDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCS
                                                                                                                              HNAQFDLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYG---------
                                                                                                                                                                         -----AEGKTPLHVAAYFGHVSLVKLLT------SQGAELDAQQRNLRTPL
                                                                                                                                                                                                                  LTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL
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                                                                                    VERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYLICKMLLR 581
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46; Mismatches 144;
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RESULT 7 US-11-317-329-37

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; TYPE: PRT ; ORGANISM: Homo sapiens US-11-317-329-38
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US-11-317-329-38
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US-11-317-329-37
                                                                                                                                                                                                                                                                                                                   Sequence 38, Applicate Publication No. US200 GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
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Best Local (
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                                                                                  SEQ ID NO 38
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APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
TITLE OF INVENTION: Methods and Compositions
FILE REPERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
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APPLICANT: Inohara, Machiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
                                                                                                        NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
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l Similarity 21.6%;
88; Conservative '
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; Pred. No. 1.6; 
46; Mismatches 144; Indels 12
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US-11-317-329-39
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 39
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 39, Application US/11317329 Publication No. US20060105413A1 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
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443
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                                                                                                                                                       338 KRALQLSDRKNLVPRDEELCIYENKVTPLQFLVAQGSVE------QVRLLLAHEVDVD 389
                                                                                                                                                                                             61 TWPVKLGE---LTPRGGELIAYLGHYW-RQRLVADGLLPKCGCPQSGQVAII----ADVD 112
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TARLLLDHGACVDA-QEREGWTPLHLAA--QNNFENVARLLVSRQADPNLRE---
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                                    ----LDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCS
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                                                US-11-317-329-41
                                                                    RESULT 11
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; ORGANISM: Homo sapiens
US-11-317-329-40
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Sequence 41, Application US/11317329 Publication No. US20060105413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 40
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/11317329 Publication No. US20060105413A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Machiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REPERENCE: UM-06967
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                                                                                                                                                        313 ----VTLPT----SVLFIAGHDTNL------ANLGGALELNWT 341
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21.6%; Pred. No. 1.6;
ative 46; Mismatches 144;
                                                                                                                                                                                            -VERGKVRAIOHLLKSGAVPDALDOSGYGPLHTAAARGKYLICKMLLR
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RESULT 12
US-11-317-329-42
is Sequence 42, Application US/11317329
publication No. US20060105413A1
GENERAL INFORMATION:
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Query Match 4.1%; Score 93.5; D
Best Local Similarity 21.6%; Pred. No. 1.6;
Matches 88; Conservative 46; Mismatches
                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
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APPLICANT: Inchara, Nachiro
TITLE OP INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR PILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
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                                                                                                      LENGTH: 765
TYPE: PRT
ORGANISM: Homo s
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TITLE OF INVENTION: Methods &
FILE REFERENCE: UM-06967
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TYPE: PRT
ORGANISM: Homo mapiens
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Pred. No. 1.6;
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                                       DB 7;
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                                         Length 765;
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US-11-317-329-43
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CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Application US/11317329 Publication No. US20060105413A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions
FILE REFERENCE: UM-06967
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 765
TYPE: PRT
ORGANISM: Homo sapiens
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                                                      TARLLLDHGACVDA-QEREGWTPLHLAA--QNNFENVARLLVSRQADPNLRE-----
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LTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSL 271
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                                                                                        ----LDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREKQDESCS
                                                                                                                           CQT-----ASGYTPLLIAAQDQQPDLCALLLAHGADANRVDEDGWAPLHFAAQNGDDR
                                                                                                                                                             ERTRKTGEAFAAGLAP-----DCAITVHTQADTSSPD-----PLFNPLKTGVCQ
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                                                                                                                                                                                                                                                                                                                                             4.1%; Score 93.5; DB 7; Length 765;
21.6%; Pred. No. 1.6;
tive 46; Mismatches 144; Indels 12
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US-11-317-329-44
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SEQ ID NO 44
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Publication No. US20060105413A1
GENERAL INFORMATION:
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CUBRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
NUMBER: OF SEQ ID NOS: 44
COUNTAINT
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582 YGASLELPTHQGWTPLHLAAYKGHLEIIHLLAESHANMGALGAVNWT
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                                                                          HLA------VERGKVRAIQHLLKSGAVPDALDQSGYGPLHTAAARGKYLICKMLLR
                                                                                                                                                     ----AEGKTPLHVAAYFGHVSLVKLLT------SQGAELDAQQRNLRTPL
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US-10-505-928-150
; Sequence 150, Application US/10505928
; Publication No. US20060088532A1
; GENERAL IMPORMATION:
; GENERAL IMPORMATION:

APPLICANT: Ludwig Institute for Cancer Research et TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178

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GURRENT APPLICATION NUMBER: US/10/505,928;
CURRENT FILING DATE: 2004-08-27;
PRIOR APPLICATION NUMBER: US 60/363,019;
PRIOR FILING DATE: 2002-03-07;
NUMBER OF SEO ID NOS: 866;
SOFTWARE: PATCHINI 3.2;
SEQ ID NO 150;
LENGTH: 5738;
TYPE: PATCHINI STORE;
ORGANISM: Homo Bapiens
US-10-505-928-150
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Search completed: June 13, 2006, 10:51:03 Job time : 10.9083 secs
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4.0%; Score 90.5; DB 6; Length 5738;
Best Local Similarity 22.9%; Pred. No. 53;
Matches 110; Conservative 35; Mismatches 159; Indels 177; Gaps
                                                                                                                                                                                                                                             2633 QPTMP----FCGEHS------LCPQGPSSVPEGHGLHSMLVEYLLFPRNWDD 2674
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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101.5	103	103.5	103.5	103.5	104.5	105	107	107.5	107.5	108	109.5	109.5	109.5	111.5	112.5	116.5	132	137	536	538	547	554	560	560	959.5	2144	2144	2182	Score	
5	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4 8	4.8	4.8	4.8	4.8	4.8	4.9	5.0	5.2	5.8	6.1	23.7	23.8	24.2	24.5		.24.8	42.5	95.0	95.0	96.6	Query Match	•
356	769	1048	888	537	397	450	5126	479	459	386	479	457	344	421	438	423	423	416	414	417	413	413	413	413	441	444	434	432	Length	
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P75594	B87681	BVECSC	T46726	S54770	C81716	A54429	S40450	JN0715	S52250	JH0610	JN0890	A56925	B89130	S14742	S64682	A33395	S06167	T16058	E87316	S25627	AG0632	JV0087	B85636	F90773	AC0201	D85633	H90770	B36733	ID	
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A;Molecule type: DNA
A;Residues: 1-50,'NAGCHPRRWANLAG',65,'T',67-74,'DV',77-111,'S' <TOU>
A;Residues: 1-50,'NAGCHPRRWANLAG',65,'T',67-74,'DV',77-111,'S' <TOU>
A;Cross-references: UNIPARC:UPIO00016BDE2; GB:X05471; NID:g40925; PIDN:CAA29031.1; PID:g.
R;Dassa, J.; Fsihi, H.; Marck, C.; Dion, M.; Kieffer-Bontemps, M.; Boquet, P.L.
Mol. Gen. Genet. 229, 341-352, 1991
A;Title: A new oxygen-regulated operon in Escherichia coli comprises the genes for a put
A;Reference number: S17958; MUID:92049231; PMID:1658895
A;Accession: S17960

A;Title: The structure of the promoter and amino terminal region of the pH 2.5 acid phose A;Reference number: A26534; MUID:87271766; PMID:3038201
A;Accession: A26534 A;Cross-references: UNIPARC:UPI000004750A; GB:AE000200; GB:U00096; NID:g2367111; PIDN:AA A;Experimental source: strain K-12, substrain MG1655 R;Touati, E; Danchin, A Biochimie 69, 215-221, 1987

A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-432 <BLAT>

Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64839

A;Status: not compared with A;Molecule type: DNA A;Residues: 1-17 <DA2>

conceptual

translation

Cross-references: UNIPARC:UPI000016FFB1; GB:S63811; NID:g238656; PIDN:AAB20286.1; PID:

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
96.5	96.5	96.5	97.5	98	98.5	99	99	99	99.5	100	100.5	101.5	101.5	101.5	101.5
4.3	4.3	4.3	<u>4</u> د	۵.	4.4	4.4	4.4	4.4	4.4	4.4	5	Б	4.5	4.5	4.5
1047	374	328	4056	1034	381	1413	969	560	234	971	425	1387	1214	789	635
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
C85535	139781	A83572	Н96599	AB0551	JH0152	D88844	T27997	F84341	F42696	T32883	D83186	A97673	AG2897	AE0064	A45266
ATP-dependent dsDN	subtilisin (EC 3.4	pyridoxal phosphat	protein F14J16.10	exonuclease SbcC [acid phosphatase (protein ZK792.1 [i	hypothetical prote	hypothetical prote	thrombin (EC 3.4.2	hypothetical prote	hypothetical prote	probable periplasm	conserved hypothet	DNA-directed DNA p	MPL-P protein prec

ALIGNMENTS

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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: H90770

A;Status: preliminary

A;Residues: preliminary

A;Residues: 1-434 <HAY>

A;Residues: 1-434 <HAY>

A;Coss-references: UNIPROT:Q8XC29; UNIPARC:UPI0000D0517; GB:BA000007; PIDN:BAE

A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                 RESULT 2
H90770
phosphoanhydride phosphorylase [imported] - Bacherichia coli (strain O157:H7, phosphosphorylase [imported] - Bacherichia coli (strain O157:H7, c;Species: Bacherichia coli (c;Date: 18-Jul-2001 #text_change 09-Jul-2004 C;Date: 18-Jul-2004 C;D
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A;Residues: 23-31,'A',33-34 <GR2>
A;Cross-references: UNIPARC:UPI0000179816
C;Comment: In addition to cAMP-mediated conaerobic conditions.
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                                                                                                                                                                                                                                                                                   R;Hayashi, T.; Makino, K.; Ohnishi, M.; gasawara, N.; Yasunaga, T.; Kuhara, S.;
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Local Similarity 98.1%;
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Pred. No. 2e-167;
0; Mismatches 8;
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Shiba, T.; Hattori,
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M.; Shinagawa,
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A;Cross-references: UNIPROT:Q8XC29; UNIPARC:UPI0000165751; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: appA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein appA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: D85633
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A;Gene: ECs1136
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A; Residues: 1-444 <STO>
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Best Local Similarity
Matches 419; Conserv
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Best Local Similarity
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GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFT 178
                                                                                                                MKAILIPFLSLLIPLTPQSAFAQS--EPELKLESVVIVSRHGVRAPTKATQLMQDVTPDA
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                                                           WPTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKT 118
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Pred. No. 2.4e-164;
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K.; Apodaca,
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A;Molecule type: DNA
A;Residues: 1-441 <KUR>
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, G;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Davies, R.M.; Davis, P.; Dougan, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
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AC0201
acid phosphatase (EC 3.1.3.2) [imported] - Yersinia pestis (strain CO92)
acid phosphatase (EC 3.1.3.2) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0201
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                                        TPHPPQKQAYGVTLPTS----VLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVF 357
                                                                                      IPLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQPDLLQRTPEVARSRATPLLDLIKTAL
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46.1%; Pred. No. 3.3e-69;
ative 67; Mismatches 153;
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bugan, G.;
Barrell,
periplasmic glucose-1-phosphatase [imported] - Escherichia coli (;Species: Escherichia coli (;Species: Escherichia coli (;Species: Escherichia coli (;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: B85336 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner,
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periplasmic glucose-1-phosphatase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: F90773
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F99773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 <HAY>
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LNEA 411
                                                               DSKANRDLMKIEYYYQSAEQLRNADALTLQAPAQRVTLELSGC-PIDADGFCPMDKFDSV
                                                                                                                              VILLASNAQAQTVPEGYQLQQVLMMSRHNLRAPLANNGSVLEQSTPNKWPEWDVPGGQLT
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                                                                                              RLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQI
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                                                                                                                                                                                                YEGFPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL----
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Shinagawa,
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09-Jul-2004 J.D.; Rose,

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A;Cross-references: UNIPROT:P19926; UNIPARC:UPI00001256FB; GB:M33807; NID:g145217; R.Blattuer, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64841
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-413 <BLAT>
                                                                                                                                                                                                                                                               glucose-1-phosphatase (EC 3.1.3.10) precursor - Escherichia coli C;Species: Escherichia coli C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 0 C;Accession: JV0087; H64841
R;Pradel, E.; Marck, C.; Boquet, P.L.
J. Bacteriol. 172, 802-807, 1990
A;Title: Nucleotide sequence and transcriptional analysis of the A;Reference number: JV0087; MUID:90130318; PMID:2153660
A;Accession: JV0087
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A;Residues: 1-413 <STO>
A;Cross-references: UNIPROT:Q8XBZ6; UNIPARC:UPI00000D0533; GB:AE005174; NID:g12514273;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: agp
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85636
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ilarity 33.3%;
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Pred. No. 3.7e-37;
73; Mismatches 174; Indels
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A;Note: optimal at low pH C;Keywords: homodimer; per F;1-22/Domain: signal sequence.
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C;Genetics:
A;Gene: agp
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C; Function:
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                                        DSKANRDLMKIEYVYÓSAEÓLRNADALTLOAPAORVTLELSGC-PIDADGFCPMDKFDSV
                                                          RLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQI
                                                                                                                            PQKQAYGVTLPTS---VLFIAGHDTNLANLGGALELN-WTLPGQPDNTPPGGELVFERWR
                                                                                                                                                                             YEGFPMDQVAWGEIKSDQQWKVLSKLKNGYQDSLFTSPEVARNVAKPLVSYIDKAL----
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                                                                                                         - VTDRTSAPKITVLVGHDSNIASLLTALDFKPYQLHDQNERTPIGGKIVFQRWH
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                                                                                                                                                                                                                                                 ---KEKQQCSLVDGKNTFSAKYQQBPGVSGPLKVGNSLVDAFTLQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 554; DB 2;
Pred. No. 1.1e-36;
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th, T.; Collet, S.; O'Gaora, P., S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Aitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov. glucose-1-phosphatase precursor (GIPase), secreted [imported] - C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AG032 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd A;Cross-references: C;Genetics: A;Gene: STY1153 A; Molecule type: DNA A;Residues: A;Status: preliminary 1-413 <PAR: UNIPARC:UPI0000059FE6; GB:AL513382; PIDN:CAD08242.1; PID:g16502289; N.R.; Pickard, ies, R.M.; Dowd, 18-Nov-2002 D.; Wain, J.; Cl , L.; White, N.; Churcher,

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A;Gene: agp
C;Keywords: periplasmic space; phosphohistidine; phosphoprotein;
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-417/Product: glucose-1-phosphatase #status predicted <MAT>
F;42/Active site: His (phosphohistidine intermediate) #status pre
F;314/Active site: His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Riccio, M.L.; Chiesurin,
submitted to the EMBL Data
A;Reference number: $25627
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$25627
$1ucose-1-phosphatase (EC 3.1.3.10) precursor - Providencia rettgeri
C;Species: Providencia rettgeri
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: $25627
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A;Molecule type: DNA
A;Residues: 1-417 <RIC>
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ALFAPIAPTWASTDNQADMYLDQVLVLSRHNLRTPIVNTGILTEVTDKKWPDWDAKSGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQSEPE-LKLESVVIVSRHGVRAP-TKATQLMQDVTPDAWPTWPVKLGELTPRGGELIAY
                                                           AGAPPGCKVNIHHOPEIGKMDPVPNPIIT-----
                                                                                             AGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTG--HY
                                                                                                                                     TTQGGALEVYMGHYFREWIDQNKLLADEL----CPTSNEDIYLYTNSLQRTIATAQFFA
                                                                                                                                                                   TPRGGELIAYLGHYWRQ-----RLVADGLLPKCGCPQSGQ-VAIIADVDERTRKTGEAFA 123
                                                                                                                                                                                                                                                   SLLIPLTPOSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGEL
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                             23.8%; Score 538; DB 2; 30.4%; Pred. No. 2.2e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.; Lombardi, G.; Satta,
Library, September 1992
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                                                           -NGSPEFKQKALAAMDDYLKGLSL
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9AAQ4; UNIPARC:UPI00000C70A0; GB:AE005673; NID:g13421731; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-414 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 LGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGEAFAAG
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                 LAGFTQIVNBA 425
                                                                           LVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCS 414
                                                                                                                                   RLAATLR----DGAAAIG-PVDARLVIIAGHDGTLASLGGLLRMEWTLPGYQPNQIQPGGA
                                                                                                                                                                       LIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPG-QPDNTPPGGE 354
                                                                                                                                                                                                                                                                                                                           RELERVINFPQSNLCLKREKQDESCSLTQALPSELKY----SADCVSLTGAVSLA
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                                                                                                                                                                                                                                                                                                                                                                                                   LAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGHYQTAF
                                                           LVFERWRR-DDGVRVVRVRFTGQSLSQLRNMTALDAKTPPLSAPVFVQGCGTATPAFDCR
                                                                                                                                                                                                             SGVTESLLMAWADGRDFAGLGWKSLDEEALTRSFFLHQAEFDLRLRTPYVARTLAGHLAD
                                                                                                                                                                                                                                                 SMLTEIFLLQQAQGMPEPGWG-RITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLD
                                                                                                                                                                                                                                                                                       EQLDALLMQCDKGPC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSTRIAVVTLATASAGAASAE--TIEKVVILSRHGVRSAMSSPERLEEASARPWPRFEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSL---LIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDLQYYEGFPADQVAWGLVDTPEKWKKLNTLKNAYQETLFTPKIIAKNVAHPILNYIDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%; Score 536; DB 2; 33.6%; Pred. No. 3.1e-35; tive 62; Mismatches 186
                                                                                                                                                                                                                                                                                       ---PPAPGKRRVFDAKPGFVDGEELAGLSGPEAFA
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acid phosphatase (BC 3.1.3.2) ACP2 precursor [validated] - human N;Alternate names: acid phosphatase, lysosomal C;Species: Homo sapiens (man) C;Date: 04-Dec-1992 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004 C;Accession: S06167; S05525; S01155
A;Reference number: S06167
A;Accession: S06167
A;Molecule type: DNA
A;Residues: 1-423 < VON>
                                                                                 R;von Figura, K. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F13D11.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te C;Accession: T16058
                                                                                                                                                                                                                               S06167
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C; Superfami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Fulton,
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                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q19390; UNIPARC:UPI000007AD42; EMBL:U40939; NID:g1072175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-416 <FUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBC
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GALELNWTLPGQPDNTPP-GGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVSADCVSLTGAVSLASMLTEI---FLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAIL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQIAWP-----GELTKRGILEEFQLG----QRLRKIYGEHFGDTYQPR-----DPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPD---
                                                                                                                                                                                                                                                                                                              NOTRVELHPHFC-SRSQNNDCTWDEFQRLVKKSRKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWVSLGAIDNCPVYGEAQRKSSEYAEVMDQMEKYDAELLQLVRNHADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTGKDNRTSASAQAMFAGFLPP-----NEDQTWNYELKWQPV------AQLTDESI 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEDFETVVRGA
                                                                                                                                                                                                                                                                                                                                                     PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIP
                                                                                                                                                                                                                                                                                                                                                                                                ESLRLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQRTPEVARSRATPLLD----LIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PISGHDINLVIIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---AWPTWPVKLGELTPRGGELIAYLGHYWRQRL----VADGLLPKCGCPQSGQVAI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRLVLLLP--FLPPV----AFG-----KLKFVQIWFRHGERTPGHYLYFPGDDLNNVDY 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PIVEAVKYNHVIDSLKVRYILQDDR-LPYPEWARGYENRILNMSFLIHDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59/3; 88/3; 138/3; 202/3; 244/1; 270/3; 312/3; 349/3; 377/1
ammalian acid phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.1%; Score 137; DB 2;
larity 21.7%; Pred. No. 0.0035;
Conservative 61; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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                                                                                   June 1989
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A;Description: catalyzes the hydrolysis of a wide range of phosphate esters (?Superfamily: mammalian acid phosphatase C;Keywords: glycoprotein; phospholistidine; phosphoprotein; phosphoric monoester hydrolase; 1-30/Domain: signal sequence #status predicted <SIG>
F;31-423/Product: acid phosphatase ACP2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:ACP2

A;Cross-references: GDB:118963; OMIM:171650

A;Map position: 11p11.2-11p11.11

A;Introns: 38/3; 70/3; 99/3; 150/3; 183/3; 213/3; 258/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI0000131FE1; EMBL:X12548; NID:g34262; PIDN:CAA31064.1; A;Note: part of this sequence, including the amino end of the mature protein, was cor C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Pohlmann, R.; Krentler, C; Duming, C.; 343-2550, 1988
A;Title: Human lysosomal acid phosphatase: cloning, expression A;Reference number: S01155; MUID:89052645; PMID:3191910
A;Accession: S01155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P11117; UNIPARC:UPI0000131FE1; R;Geler, C.; von Figura, K.; Pohlmann, R.

Eur. J. Biochem. 183, 611-616, 1989
A;Tille: Structure of the human lysosomal acid phosphatase
A;Reference number: S05525; MUID:89377828; PMID:2776754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;41/Active site: Arg #status predicted F;42/Active site: His (phospholistidine intermediate) #status predicted F;92,133,1ve site: His (phospholistiding site: carbohydrate (Asn) (coval F;92,133,167,197,191,267,322,331,181nding site: carbohydrate (Asn) (coval F;159-370,212-310,345-349/Disulfide bonds: #status predicted
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A; Residues: 1-423 < POH>
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A; Residues: 1-29 < GEI>
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                                                                                                                                                                                                                                                                                                                       QDESCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFL------LQQAQGMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADGLLPKCGCPQSGQVAIIADVD-ERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRFVTLLYRHGDRSPVKT----YPKDPYQEEEWPQGFGQLTKEGMLQHWELGQALRQRY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGELTPRGGELIAYLGHYWRQRLV
                                         VSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIP
                                                                                         ---LP-KLLVYSAHDTTLVALQMALDVY-----NGEQAPYASCHIFELYQEDSGN---FS
                                                                                                                                    GVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVPERWRRLSDNSQWIQ 371
                                                                                                                                                                                  PW---ASPQTMQRLSRLKDFSFRFLFGIYQQAEKARLQGGVLLAQIRKNLTLMATTSQ--
                                                                                                                                                                                                                           GWGRITDSHQWNTLLSLHNAQFDLL---QRTPEVARSRATPLLDLIKTALTPHPPQKQAY
                                                                                                                                                                                                                                                                           QNE----TROTPEYQNESSRNAQFLDMVANETGLTDLTLETVWNVYDTLFCEQTHGLRLP
                                                                                                                                                                                                                                                                                                                                                                       FNPNISWQPIPVHTVPITE-----
                                                                                                                                                                                                                                                                                                                                                                                                                FNP-LKTGVCQLDNANVTDAILERAGGSIADFTGHYQTAFRELERVLNFPQSNLCLKREK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -HGFL---NTSYHRQEVYVRSTDFDRTLMSAEANLAGLFP
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-RNESDKAPWPLSLP------
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Pred. No. 0.009
43; Mismatches
-GCPHR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
0.0091;
                                                                                                                                                                                                                                                                                                                                                                    -----DRLLKFPLGPCPRYEQL
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-CPLQDFLRL-TEPVVP
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acid phosphatase (EC 3.1.3.2) precursor -C;Species: Rattus norvegicus (Norway rat) C;Date: 29-Jan-1990 #sequence_revision 29-C;Accession: A33395

t) 29-Jan-1990

#text_change 09-Jul-2004

A33395

RESULT

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acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal C;Species: Drosophila melanogaster
C;Date: 06-Dec-1996 #sequence revision 06-Dec-1996 #text_C;Accession: $64682; $64681
R;Chung, H.J.; Shaffer, C.; MacIntyre, R.
Mol. Gen. Genet. 250, 635-646, 1996
A;Title: Molecular characterization of the lysosomal acid A;Reference number: $64681; MUID:96194627; PMID:8676866
A;Accession: $64682
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C;Keywords: phosphohlatidine; phosphoprotein; phosphoric monoester hydrolase
F;41/Active site: Arg #status predicted
F;42/Active site: His (phosphohlstidine intermediate) #status predicted
                 A;Cross-references: UNIPARC:UPI000017595EC;Genetics:
                                                     A; Molecule type: mRNA
A; Residues: 1-31,'Y', 33-438 < CHW>
                                                                                                        A;Cross-references: UNIPROT:Q9VAD0; A;Accession: S64681
                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-438 < CHU>
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                                                                                     A; Status: not compared with
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A; Residues: 1-423 < HIM>
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Best Local
FlyBase:Acph-1
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Pred. No. 0.16,
46; Mismatches
                                                                                                                         UNIPARC: UPI000017595D
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RESULT 15
S14742
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R;Geier, C.; von Figura, K.; Pohlmann, R.
Biol. Chem. Hoppe-Seyler 372, 301-304, 1991
A;Title: Molecular cloning of the mouse lysosomal acid; A;Reference number: S14742; MUID:91282986; PMID:205937
A;Accession: S14742
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C;Superfamily: mammalian acid phosphatass
C;Keywords: phosphoric monoester hydrolase
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-438/Product: acid phosphatase Acph-1 #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-421 <GEI>
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                                                                                                                                                                                 2 KAILIPF-----LSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTP
                                                                                                                                                                                                                          l Similarity
98; Conserv
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                                   RKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIA 175
LMSAEANLAGLFPP-----NEVQHFSPNISWQPI-----PVHTVPITE
                                                                                                                                               QAALLQFLLGMCLTVMPPIQARS--
                                                                      YQEEKWPQGFGQLTKEGMLQHWELGQALRQRY--HGFL---NTSYHRQEVYVRSTDFDRT
                                                                                                          DAWPTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVD-ERT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYNMTLPKWTKKVYGREELTYVS--NFAFAISSYTRKLARLKAGPLLKDIFQRF-----
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21.4%; Pred. No. 0.4;
vative 53; Mismatches 171;
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Pred. No. 0.3
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                                                                                                                                                                                                                        Indels 137;
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Search completed: June 13, 2006, 10:29:30 Job time: 26.2661 secs

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Result
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Maximum DB
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-MODEL-frame+ p2n.model -DEV-xlh
-Q=/abss/ABSSWEB_spool/US10601319/runat 12062006_180050_27480/app_query.fasta_1
-Q=/abss/ABSSWEB_spool/US10601319/runat 12062006_180050_27480/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000 -HOST=abss06h
-USER=US10601319 @CGN 1 1 3991 @runat 12062006 180050 27480 -NCPU=6 -ICPU=3
-NO_MAAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -LONGLOG -FGAPDEXT=7
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AR636190 Sequence
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ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
                                               Alignment Scores: Pred. No.:
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Short,J.M., Kretz,K.A., Gray,K.A., Barton,N.R., Garrett,J.B., O'Donoghue,E. and Mathur,E.J.
Recombinant bacterial phytases and uses thereof patent: US 685535-A 7 15-FEB-2005;
Diversa Corporation, San Diego, CA
                                                                                                                                                                                                                                                                                                                                  Sequence 7 from patent US 6855365.
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AR636190.1 GI:62768873
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               PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
                                                    LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                                               ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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                                                                                   CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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Short, J.M., Kretz, K.A., Gray, K.A., Barto O'Donoghue, E. and Mathur, E.J.

O'Combinant bacterial phytases and uses Patent: US 685365-A 9 15-FEB-2005;

Diversa Corporation; San Diego, CA Location/Qualifiers
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GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120
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Recombinant bacterial phytases and Recombinant of 1999 Patent: WO 0190333-A 7 29-NOV-2001, DIVERSA CORPORATION (US)
Location/Qualifiers
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                  TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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                                    LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
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O'Donoghue,E.
Recombinant bacterial phytases and uses
Patent: WO 0190333-A 9 29-NOV-2001;
DIVERSA CORPORATION (US)
                                                                                                                                                                                                                                                     AX356574
Sequence 9 from Patent 1
AX356574
AX356574.1 GI:18621060
                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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Alignment Scores: Pred. No.: 2.74e-196 Percent Similarity: 98.18 Conservative: 0	04 changed to G			/Brandard name="HI/N murant" /notes "created by site directed mutagenesis" /citation=[2] variation 11631165 /gene="appA" /standard name="D304A murant"	yeara-	ion	variation appA und variation	variation 299, .301 /gene="app /standard /note="cre /citation=	-2002 sig_peptide mat_peptide	420 //protein id="AAA72086; /db xref="GI:145285" /translation="MKAILIPF /translation="MKAILIPF TKATQLMQDVTPDAMPTWPVKI GQVALIADVDERTRKTGBAFAAF NVTDAILSRAGGSIADFTGHRG ELKVSADNVSLTGAVSLASMIJ	1387	RBS 172177 380 /gene="appA" 1327 /gene="appA" 1327 /gene="appA"	1267

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Forsberg,C.W., Golovan,S. and Phillips,J.P.
Transgenic animals expressing salivary proteins
Patent: WO 0064247-A 5 02-NOV-2000;
UNIVERSITY OF GUELPH (CA)
Location/Qualifiers
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Sequence 5 from Patent |
AX042376
AX042376.1 GI:11340994
                                                     ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG
             GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                                                                                               GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
                                                                                                                              ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
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/db_xref="taxon:32630"
/noTe="R15/APPA transgene"
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                                                                                 CTGGCAGGATGTGAAGAGCGAAATGCGCAGGGCATGTGTTCGTTGGCAGGTTTTACGCAA
                                                                                          LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
                                                                                                                     CAGATGCGTGATAAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC 3010
                                                                                                                                 GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400
                                                                                                                                                         ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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                                             ATCGTGAATGAAGCACGCATACCCGCTTGCAGTTTG
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Transgenic animals expressing salivary proteins
Patent: WO 0064247-A 3 02-NOV-2000;
UNIVERSITY OF GUELPH (CA)
Location/Qualifiers
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       MetlysalaileLeuileProPheLeuSerLeuLeuileProLeuThrProGlnSerAla
                                                                                AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                                                                                                                   TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
                                                                                                                              SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
                                                                                                                                                       AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr
                                                                                                                                                                                                       GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
                                                                                                                                                                                                                                             GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
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                                                      TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                                                                                                                             CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
                                                                                                                                                                                                                                                                                                           GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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/mb xref="taxon:32630"

/noTe="R15/APPA + intron transgene"
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Alignment Scores: Pred. No.: 2.07e-195	a rõ	TITLE Transgenic animals expressing salivary proteins JOURNAL Patent: WO 0064247-A 4 02-NOV-2000; UNIVERSITY OF GUELPH (CA) FEATURES Location/Qualifiers	NISM synthetic of other sequence 1	AX042375 AX042375.1 GI:1134099:	RESULT 8 AX042375 AX042375 AX042375 AX042375 AX042375 DIA linear PAT 23-NOV-2000 DEFINITION Semience 4 from Parent WODD64247.	Qy 421 IleValAsnGluAlaArgIleDroAlaCysSerLeu 432	Qy 401 LeualaglyCysGluGluArgAsnAlaGlnGlyMetCysSexLeualaGlyPheThrGln 420	Qy 381 GlmMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr 400	Qy 361 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380	Qy 341 ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGlyGluLeuValPheGluArgTrp 360	Qy 321 PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	Qy 301 LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320	Qy 281 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300	Qy 261 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln 280	Qy 241 GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGlyTrpGlyArgIleThr 260	Qy 221 LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240
Qy 321 PheIleAlaGlyHisAspThrAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340	Oy 281 ArgTh:ProGlivalA.aArgserArgAlain:ProLeuLeuAspLeulleuSight and 1900	261 ABpSerHisGlnTrpAsnThrLeuLeuSerLeuHißAsnAlaGlnPheAspLeuLeuGln	Qy 241 GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGlyTrpGlyArgIleThr 260	Qy 221 LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240	Qy 201 LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220	Qy 181 TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200	Qy 161 ASNVAlThrASPAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180	Qy 141 SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160	Qy 121 AlapheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140	Qy 101 GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120	Qy 81 GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro 100	Oy 61 ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80	Qy 41 ValargalaProThrLysalaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	Qy 21 PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40	Qy 1 MetLysAlaIleLeuIleProPheLeuSerLeuIleProLeuThrProGlnSerAla 20	DB: 2 Gaps: 0 US-10-601-319-10 (1-432) x AX042375 (1-6116)

& & &	B 8 B 8	B 8 8	-10-6	Best Loc Query Ma DB:	Alignment Pred. No. Score: Percent S	ORIGIN		TITLE JOURNAL	ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 9 AX042373 LOCUS DEFINITION	D 99	g Q	8 8	D QY	ъ
81 GlyHisTyrTxpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro 	41 ValArgAlaProThrLy6AlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro 60	1811 ATGAAAGCCATCTTAATCCCATTTTTATCTCTTCTGATTCCGTTAACCCCGCAATCTGCA 1870 21 PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40	-10 (1-432) x AX042373 (1-6708) MetLysAlaIleLeuIleProPheLeuSerLeuIleProLeuThrProGlnSerAla	rity: 98.1% Mismatche 96.6% Indels: 2 Gaps:	2.37e-195 Length: 2182.00 Matches: 98.1% Conservative:	/db_xret="taxon:32630" /noTe="R15/APPA + intron plasmid with pBLCAT3 vector"	rce	Transgenic animals expressing salivary proteins L Patent: WO 0064247-A 2 02-NOV-2000; UNIVERSITY OF GUELPH (CA) TOCATION (701)1fiars	3	AX042373 GI:11340991	ž	421 IleValAsmGluAlaArgIleProAlaCysSerLeu 432 	401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420 	381 GlametArgAspLysThrProLeuSsrLeuAsnThrProProGlyGluValLysLeuThr 400	361 ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380 	
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Transgenic animals expressing salivary proteins
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Short, J.M., Kretz, K.A., Gray, K.A., Ba
O'Donoghue, E. and Mathur, E.J.
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Patent: US 6855365-A 5 15-FEB-2005;
Diversa Corporation, San Diego, CA
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1448 ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG 1483	421 IleValAsnGluAlaArgIleProAlaCysSerLeu 432	1388 CTGGCAGGATGTGAAGAGCGAAAATGCGCAGGGCATGTGTTCGTTC	401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420	

Search completed: June 14, 2006, 13:55:38 Job time: 5313.22 secs

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Result
No.
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-[abse]ABSSWEB gpool/US10601319/runat 12062006_180047_27417/app_query.fasta_1
-Q-[abse]ABSSWEB gpool/US10601319/runat_12062006_180047_27417/app_query.fasta_1
-DB=N Geneseq -QFMT=fastap -SUPFIX=rng -MINMATCH=0.1 -LZOPCL=0 -LZOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR _SCORE=pct -THR_MAX=100 -THR _MIN=0 -ALIGN=15 -MODE=LOCAL
-UNITFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abse06h
-USER=US10601319_@CGN 1 1 749_@runat 12062006_180047_27417 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPELCCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XAAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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seq length: 2000000000
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2: geneseqn20
3: geneseqn20
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Aed50817 Escherich
Adc87742 DNA encod
Ado50299 Escherich
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PRINCE FOR THE FOREST CONTRACTOR OF THE FOREST

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RESULT 1
AED50817
ID AED5
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                                                                                                                                                                           Transgenic animal; gene therapy; feedstuff; food; thermostable; mutant; ds; coding sequence; 3-phytase; recombinant DNA; appA gene.
                                                                                                                                                                                                                  Escherichia coli phytase appA mutant DNA SEQ ID NO: 1 #1.
US2005246780-A1
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                                    /EC_number= "3.1.3.8"
/partial
/product= "Escherichia coli phytase mutant protein"
                                                                                                        Location/Qualifiers
                          note= "No stop codon"
                                                                               *tag=
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Aad57148 pNOv4054
Aed46569 Nov9x phy
Aad57149 pNOv4058
Aec39118 pNOv4061
Ad102197 DNA encod
Aad06831 E. coli a
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Aac68394 Lama2/APP
Ad16139 Shigella
Aee75417 E. coli p
Ad050303 Escherich
Aac8885 Escherich
Aad36473 Escherich
Aad25460 Escherich
Add25460 Escherich
Add19445 E. coli B
Ad0550291 Escherich
Aee75412 E. coli B
Ad050301 Kangaroo
Aed46567 Nov9x phy
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Ada1949 E. coli K
Adc87744 DNA encod
Adc80297 Escherich
Aed50819 Escherich
Aed50819 Escherich
Aed57418 E. coli B
Aac68298 R15/APPA
Aac68297 R15/APPA
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Aee75422 E. coli B
Ado50296 Escherich
Ado50295 Escherich
Aee75416 E. coli p
Abk12514 DNA encod
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Acf35789 Nov9X phy
Ada19452 E. coli K
Aac68299 SV40/APPA
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Adl16137 Escherich
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01-MAR-1999;

13-APR-1999;

25-MAY-1999;

25-MAY-2000;

24-MAY-2001;

24-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a recombinant phytase (EC 3.1.2.8) protein and its encoding also nucleic acid molecule. Phytases of the invention is a thermostable protein. They are useful in foodstuffs, for oil degumming, producing an animal feed, delivering a phytase enzyme supplement to an animal, increasing the resistance of a phytase polypeptide to enzymatic inactivation in a digestive system of an animal and in processing of corn and sorghum kernels. The invention is also useful in gene therapy and in production of transgenic animals. The present sequence is the SEQ ID NO: 1 which is given in the sequence listing. This sequence differs from the SEQ ID NO: 1 shown on page 19 in disclosure of the specification (see AED50824).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Short JM,
Mathur EJ;
                                                                                                                                                                                                                                                                                                                                                                Sequence 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated or recombinant nucleic acid encodi as foodstuff, and for oil degumming, producing a phytase enzyme supplement to an animal.
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(GRAY/)
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(ODON/)
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) ODONOGHUE E.
) MATHUR E J.
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                                                                                          ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
                                                                                                                                           PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
                                                                                                                                                                                             MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla
GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                         ThrTrpProValLy8LeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
                                                                                                                              TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
                                                                                                                                                                                 ATGAAAGCGATCTTAATCCCATTTTTATCTCTTGATTCCGTTAACCCCGCAATCTGCA
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2001US-00866379.
2002US-00156660.
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                                                     IleValAsnGluAlaArgIleProAlaCysSerLeu
                                                                                                                                                          GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                                                                                                                                                            CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                                                                                                                                                                ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
                                                                                                                                                                                                                                                                                                                 PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
                                                                                                                                                                                                                                                                                                                                                                   LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
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                                       ATCGTGAATGAAGCACGCATACCGGCGTGCAGTTTG
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                                                                                                       LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
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The invention discloses a new isolated or recombinant nucleic acid which concluded a polypeptide having a phytase activity. Also claimed is a nucleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic concluded an antisense oligonucleotide, inhibiting the translation of a second domain, an array comprising immobilised polypeptide or nucleic acid, a hybridoma comprising an antibody that specifically binds to the polypeptide, a food supplement for an animal, an edible enzyme delivery matrix, an edible pellet comprising a granule edible enzyme delivery polypeptide, a feed composition, a soybean meal, isolating or identifying the polypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, determining whether a compound binds to the polypeptide, plantifying a medilator, whole cell engineering of new or modified therefore the resistance or thermostability of the phytase polypeptide, increasing the resistance of the phytase polypeptide to enzymatic inactivation in a citivity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or encoding the modified Escherichia coli phytase.
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000; 20
24-MAY-2001; 20
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improving the feeding value of phytate rich ingredients or as an aid
phytate digestion.
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LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                        GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTGATTTGCTACAA
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                                       ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC improve the feeding value of phytase enzyme can be used in foodstuffs to CC improve the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1308 BP; 315 A; 345 C;
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Mather EJ;
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                                                             GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
                                                                                               GGACATTACTGGCGTCAGCGTCTGGTAGCCGACGGATTGCTGCCTAAATGTGGCTGCCCG
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ds; coding sequence; mutant; thermostable; phytase;
protein stabilization; pharmaceutical; fertilizer;
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E. coli B

(first

entry)

modified appA phytase 819PH59 DNA sequence

SEQ ä SO:

cramp; cell culture;

AEE75420; AEE75420

DNA; 1308

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                             IleValAsnGluAlaArgIleProAlaCysSerLeu 432
                                                                                                                                                CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
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Alignment Scores: Pred. No.:
                                                                          The present sequence is that of a polynucleotide encoding a novel composition phytase derived from the Escherichia coli appA protein, with coli improved thermal tolerance and protease stability compared to the wild-cype. The present invention relates to a novel formulation, comprising at colleast one polypeptide having phytase activity, where the polypeptide is a composition sequence (AEE75419). The modification of the enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of the protein. The specification also claims a pharmaceutical composition, con a kit; an immobilized phytase; a fertilizer or soil additive; a liquid culture or cell culture media; and a plant food additive, all comprising the novel phytase, and a method of reducing pollution and increasing culture or cell culture media; and a plant food additive, all comprising contrient availability in an environmental enzyme is a dietary complement useful for treating, preventing or reversing osteoporosis or sone loss, and preventing muscle cramps. The liquid supplement is useful for treating muscle cramps. The liquid supplement is useful for preventing muscle cramps. The liquid supplement is useful for reducing pollution and increasing nutrient availability in an environment or environmental sample comprises a soil or a body of water. The immobilized comprises is useful in foodstuffs for improving the feeding value of comprises a soil or a body of water. The immobilized phytate rich ingredients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1997;
01-MAR-1999;
13-APR-1999;
                                                  Sequence 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Formulation useful as dietary supplement for treating, preventing creversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
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BARTON N R.

GARRETT J B.

ODONOGHUE E.

BAUM W.

ROBERTSON D
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2000US-00580515.
2001US-00866379.
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99US-00259214.
99US-00291931.
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1. .1296
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Best Local Similarity:
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pharmaceutical;
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/note= "Wild type l
replace(477,A)
/*tag= k
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replace(439,A)
/*tag= g
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                           /note= "Wild type
replace(476,A)
/*tag= j
                                                       replace(472,G)
/*tag= i
                                                                                                                                                /note= "Wild type
replace(438,A)
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replace(470,G)
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replace(437,C)
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  The present sequence is that of a polynucleotide encoding a novel modified phytase derived from the Escherichia coli appA protein, with improved thermal tolerance and protesses stability compared to the wild-type. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity, where the polypeptide is a modified sequence (AEE75421) derived from the Escherichia coli K-12 appA
                                                                              Formulation useful as dietary supplement for treating, preventing or reversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
                                                                Claim 1, Page; 82pp; English.
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25-MAY-2000;
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13-APR-1999;
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(BART/)
(GARR/)
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DB; AEE75421.
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KRETZ K A.
GRAY K A.
BARTON N R.
GARRETT J B.
ODONOCHUE E.
                                                                                                                                                                           BAUM W.
ROBERTSON
ZORNER P.
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2000US-00580515.
2001US-00866379.
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replace(1016,T)
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99US-00291931.
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RESULT 5
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CC phytase (AEE75419). The modification of the enzyme, comprising a series of mutations, improves the thermal tolerance and protease stability of CC the protein. The specification also claims a pharmaceutical composition, CC a kit, an immobilized phytase; a fertilizer or soil additive; a liquid CC supplement for preventing muscle cramps; a hydrating agent; a tissue CC culture or cell culture media; and a plant food additive, all comprising CC the novel phytase, and a method of reducing pollution and increasing CC nutrient availability in an environment or environmental sample by CC degrading environmental phytic acid. The novel enzyme is a dietary Supplement useful for treating, preventing or reversing osteoporosis or CC bone loss, and preventing muscle cramps. The liquid supplement is useful CC for preventing muscle cramps. The method is useful for reducing pollution CC and increasing nutrient availability in an environment or environment or CC environmental sample comprises a soil or a body of water. The immobilized CC phytase is useful in foodstuffs for improving the feeding value of CC phytase is useful in foodstuffs for improving the feeding value of CC specification but was created from the wild-type sequence (AEE75418) and CC the information given in claim 1.
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DB:
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Best Local Similarity:
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                                                                                   TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                                                                                                                                AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                                                                                                                                                                                                                                                                                                            SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160
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LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
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                                                   TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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CC The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to CC modified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to CC mumerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as chicken, ducks, doves, parrot, etc., CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC etc., in dough making and baking, in dietary aids for animals. The method CC provides easy manufacture of the active ingredient loaded biocompatible CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase mutant DNA.
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Best Local Similarity:
Query Match:
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25-MAY-2000;
24-MAY-2001;
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) KRETZ K.
) GRAY K A.
) BARTON N R.
) GARRETT J B.
) O'DONOGHUE B.
) MATHER E J.
                                                                                                                                                  ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80
                                                             ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
                                                                                                                PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g phytase, involves providing nucleic acid derived
polypeptide having phytase activity, and expressir
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99US-00291931.

99US-00318528.

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                    IleValAsnGluAlaArgIleProAlaCysSerLeu
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                                        The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to condified phytase enzyme which has improved thermal tolerance and protease CC stability at low pH. The phytase enzyme can be used in foodstuffs to comprove the feeding value of phytate rich ingredients, and in diet of CC numerous animals including mammals, fowls and fishes, commercially CC significant mammals such as pigs, goats, laboratory rodents, commercially CC significant avian species such as guppy, zebrafish, molly, swordtail, CC commercially farmed fish such as guppy, zebrafish, molly, swordtail, CC composition, higher yields and loading efficiency. The phytase CC composition, higher yields and loading efficiency. The phytase CC incorporated in to the dietary aid is safe for animals. The present CC sequence is Escherichia coli K12 appA phytase mutant DNA.
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25-MAY-1999;
25-MAY-2000;
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Mather EJ;
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(GARR/)
(ODON/)
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KRETZ K.
GRAY K A.
BARTON N R.
GARRETT J B.
O'DONOGHUE E.
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al feed; fish feed; dough; ba)
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LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                                                                                                            GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
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                                                                                                                                                                                                                                                                                                                    TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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                                                        ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
                                                                                                           AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
                                                                                                                                                                                                                                                                                                    CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                                                                                                                                                                                                                                                                     AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
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                                         CGCACGCCAGAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
                                                                                           GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                                                                              GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
                                                                                                                                                                                               AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1997;
01-MAR-1999;
13-APR-1999;
             Formulation useful as dietary supplement for treating, preventing creversing osteoporosis and bone loss, and preventing muscle cramps, comprises one or more polypeptides having phytase activity.
                                                                                                                                                       Short J
Baum W,
                                                                                                                                                                                                                                                                  (GARR/)
(ODON/)
(BAUM/)
                                                                                                                                                                                                                                                                                                                                     (KRET/)
(GRAY/)
(BART/)
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25-MAY-2000;
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                                                                                                                                                                                                                                                               SHORT J M.

KRETZ K A.

GRAY K A.

BARTON N R.

GARRETT J B.

ODONOGHUE E.

BAUM W.
                                                                                                                                                                                                                          ROBERTSON D
ZORNER P.
                                                                                                                                                    , Kretz KA,
Robertson DE,
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2000US-00580515.
2001US-00866379.
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99US-00291931.
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Best I Query DB:

Percent Similarity:
Best Local Similarity:
Query Match:

1.45e-195 2190.00 98.4% 98.4% 97.0%

Length:
Matches:
Conservative:
Mismatches:
Indels:

1901 425 0 7 0

Gaps:

Pred.

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Alignment Scores:

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The present sequence is a DNA sequence related to the production of the CC movel thermostable / protease resistant Escherichia coll phytase CC described in the specification. The present invention relates to a novel formulation, comprising at least one polypeptide having phytase activity. CC where the polypeptide is a modified sequence (AEE7542) derived from the Escherichia coll K-12 appA phytase (AEE7541). The modification of the CC enzyme, comprising a series of mutations, improves the thermal tolerance CC and protease stability of the protein. The specification also claims a CC pharmaceutical composition; a kit; an immobilized phytase; a fertilizer or soil additive, a liquid supplement for preventing muscle cramps; a CC hydrating agent; a tissue culture or cell culture media; and a plant food additive, all comprising the movel phytase, and a method of reducing CC pollution and increasing the movel phytase, and a method of reducing CC enzyme is a dietary supplement useful for treating, preventing or creversing osteoporosis or bone loss, and preventing muscle cramps. The CC enzyme is a dietary supplement useful for treating, preventing or creversing osteoporosis or bone loss, and preventing muscle cramps. The CC inquid supplement is useful for preventing muscle cramps. The mention or environmental sample by degrading environmental phytic acid, where the environment or environmental sample comprises a soil or a body of water. The immobilized phytase is useful in foodstuffs for improving the feeding value of phytate rich ingredients. NOTE: The CC present sequence is shown in the sequence listing but not discussed cc elsewhere in the specification.
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Sequence 1901 BP; 475 A; 499 Ç 499 ç, 427 Ŧ, 0 U; 1 Other,

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                                                       SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
                                                                                                                                                          GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu
                                                                                                                                                                                                               GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
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                                                                                         GCCTTCGCCGCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                                                                                                           CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAA
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Unidentified
                                                                                  Phytase; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel phytase gene, recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-645078/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1299 BP; 317 A; 345
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                                                                                                                  GCCTTCGCCGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
                                                                                                                                                          GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120
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                                                                                     SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
                                                                                                         Escherichia coli.
                                                                                                                              drug design; gene.
                                                                                                                                                                  Prokaryotic essential gene
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                                  21-MAR-2002; 2002WO-US009107
                                                                                WO200277183-A2
                                                                                                                                           Antisense; ds; prokaryotic essential gene; cell proliferation;
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense curcleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of identifying a per proliferation, or that inhibits cellular proliferation or proliferation, or that inhibits cellular proliferation of a proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, C. prokundown and the printed specification, but was obtained in the target or prokundown and cellular proliferation in cells other than S. aureus, S. typhimurium, C. prokundown and the printed specification, but was obtained in the target or prokundown and the printed specification, but was obtained in
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Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; SEQ ID NO 7167; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                     ftp.wipo.int/pub/published_pct_sequences
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Trawick JD,
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Carr GJ,
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Forsyth
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Sequence 1299 BP; 317 A; 345 ũ 355 G; 282 ij 0 U; 0 Other;

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Db 121 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA 180		Db 61 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT 120	Qy 21 PheAlaGinSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40	Db 1 ATGAAAGCGATCTTAATCCCATTTTTATCTCTGATTCCGTTAACCCCGCAATCTGCA 60	
ATGGCCA	aTrpPro	TCATGGT	gHisGly	ATCTGCA	nSerAla
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LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
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                                                                                                                                                                ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380
                                                                                                                                                                                                                                    ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp 360
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Mrachko GT,
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I, Schellenberger
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Novel recombinant phytase having modified phytase activity comprising modification of amino acid residues in mature Escherichia coli phytase designated EBC18B2, useful as feed additive.

Claim 19; Fig 21; 107pp; English.

The invention relates to recombinant modified AppA phytases having CC modified phytase activity. The AppA phytases are derived from a mature Escherichia coll AppA phytase designated EBC18B2 (see ADL16120), and CC comprise substitutions at least one of residues 26, 43, 46, 54, 73, 113, CC 126, 184, 228, 384 or 410, or at a residue located within 5 residues of CC those listed above. The invention also encompasses polymucleotides encoding a modified AppA phytase and which further encodes a secretion CC signal sequence operable in Bacillus sp.; expression constructs, vectors and host cells (preferably Bacillus subtiliss) comprising the CC polymucleotide sequences; and an method for the production of the modified AppA phytases. The invention also discloses a method of producing an CC enzyme having phytase activity; a method of producing a heterologous college of phypeptide having phytase activity in Bacillus subtilis; reducing the CC level of phosphorus in animal manure; a composition comprising a modified AppA phytase; and animal feed comprising cells, spores or plant parts, CC including seeds, capable of expressing a modified AppA phytase. The conditied AppA phytase are useful as an animal feed additive, particularly in feeds for non-ruminant livestock such as pigs and poultry which lack the digestive enzymes for extracting phosphorus from phytate (monoritations. For example, they can be used in the isolation and comprising comprises also have many other agricultural, industrial, medical and nutritional and comprises of phytases for example, they can be used in the isolation and recovery of rare metals to produce lower phosphate homologs of phytate

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which may be used in toothpaste and other dental care products as well as potential treatments or preventatives of bone resorption (e.g., in osteoporosis) and renal calculi (kidney stones); in food production (e.g., tofu and nutritional supplements); in wet grain milling; in cleaning, personal care, medical and nutritional products; in rust removal products; and in the removal and other polycations from such diverse materials as waste products and carbonated beverages. The present sequence represents Escherichia coli strain K-12 AppA phytase
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WPI; 2002-083108/11.
P-PSDB; AAE15807.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC KIZ appA phytase. The enzyme has phytase activity and improved thermal C tolerance when compared with wild-type phytase. It has improved protease c stability at low pH. The recombinant phytase is useful for improving the nutritional value of phytase-containing foodstuffs and subsequently c improving the growth performance of an organism that consumes it, in c treating animal digestive systems, in feed treatment processes and for in c vitro purposes related to research, discovery and development. They are c also used for generating recombinant digestive system life forms, for c producing or manufacturing alcoholic and non-alcoholic drinks based on c the use of moulds, grains and/or plants, in biopulping and bio- bleaching where a reduction in the use of environmentally harmful chemicals that c are traditionally used in the pulp and paper industry is desired and in c supplements, enzymes or therapeutic drugs for animals from the daily feed thus increasing the amount calories and nutrients present in the feed. C The present sequence is a DNA encoding E. coli appA phytase wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New bacterial phytase for e.g. improving the nutritional value of phytate -containing foodstuffs and subsequently improving the growth performance of an organism that consumes it, or in treating animal digestive systems.
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               AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
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AACGTGACTGACGCGATCCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCAT
                                                                 TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG
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/product= "Phytase"

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The invention relates to an isolated Escherichia coli polynucleotide cc encoding a phytase enzyme appearing as ADA19450 and having amino acids condification from W68E, Q84W, A95P, K97C, S168E, R180Y, N226C or Y277D. CC Also included the E. coli appA gene ADA19449 (or an oligonucleotide containing foodstuff by contacting nutritional value of a phytate-cc containing foodstuff by contacting the phytase-containing foodstuff and the phytase enzyme mutated phytase (where the phytase enzyme catalyzes the liberation of inorganic phosphate from the phytase enzyme catalyzes containing foodstuff), a method to produce an animal feed containing a microbial phytase (comprising culturing the plant cell, plant part or containing the plant cells, plants or plant into a composition for animals (comprising the plant seeds, plant cells, plants or plants in admixture with a phytate-containing codestuff), a method to treat a human or an animal able to benefit from the plant parts or plants in admixture with a phytate-containing comprising administering to the human or animal the plant seeds, plant cells, plant parts or plants of a transgenic plant which is modified to convertising the plant sor a transgenic plant which is modified to convertising a heterologous nucleic acid sequence encoding a phytase enzyme, a transgenic non-human organism whose genome comprising a heterologous nucleic acid sequence encoding a polypeptide having phytase activity. The phytate enzyme is useful for improving the converted method improves thermal tolerance and protease stability. It calso improves the feeding value of phytate rich ingredients. The present sequence represents the E. coli kil appA gene encoding wild-type phytase.
                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                  Alignment
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O' Donoghi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated Escherichia coli polynucleotide encoding a modified phytase enzyme, useful in the production of animal feed, for improving the nutritional value of phytate-containing foodstuff and for enhancing
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BARTON N R.
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O' DONOGHUB
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                                                             TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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CTTTACCGGGCAT

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607 140 120 487 100 427 80 367 307 40 247 20

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US-10-601-319-10 (1-432) x ADA19449

(1-1901)

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The invention discloses a new isolated or recombinant nucleic acid which encodes a polypeptide having a phytase activity. Also claimed is a nucleic acid probe, an amplification primer sequence pair, an expression cassette comprising the nucleic acid, a vector comprising the nucleic acid, a transgenic non-human animal or plant, or its seed, comprising the nucleic acid, an antisense oligonucleotide, inhibiting the translation of a phytase message in a cell, a heterodimer comprising the polypeptide and
                                                                                                                                     New nucleic acid encoding a polypeptide having phytase activity, useful in improving the feeding value of phytate rich ingredients or as an aid in phytate digestion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytase; food supplement; enzyme delivery matrix; soybean meal; thermotolerance; thermostability; kernel; phytate; myo-inositol-hexaphosphate; inositol; inorganic phosphate; thermotolerant; feed value; digestion; gene; ds; appA.
                                                                                                           Example 1; SEQ ID NO 3; 113pp; English.
                                                                                                                                                                                            P-PSDB;
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                                                                                                                                                                                                                                                  Short JM,
                                                                                                                                                                                                                                                                             (DIVE-) DIVERSA CORP.
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24-MAY-2001;
                                                                                                                                                                                                                                                                                                                                  25-MAY-1999;
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13-APR-1999;
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DB; ADC87745.
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                                                                                                                                                                                                                                                  Kretz K,
                                                                                                                                                                                                                                                                                                     ; 97US-00910798.
; 99US-00259214.
99US-00291931.
; 99US-00318528.
; 2000US-00580515.
; 2001US-00866379.
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transl_except= (pos:401.
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                                                                                                                                                                                                                                                  Gray KA,
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28888888888888888888888
                                                                                                                 CC a second domain, an array comprising immobilised polypeptide or nucleic cc acid, a hybridoma comprising an antibody that specifically binds to the CC polypeptide, a food supplement for an animal, an edible enzyme delivery CC matrix, an edible pellet comprising a granule edible carrier and the CC polypeptide, a feed composition, a soybean meal, isolating or identifying CC the polypeptide, making an anti-phytase antibody, producing a recombinant CC polypeptide, determining whether a compound binds to the polypeptide, ci dentifying a modulator, whole cell engineering of new or modified CC phenotypes by using real-time metabolic flux analysis, increasing CC the resistance of the phytase polypeptide to enzymatic inactivation in a CC digestive system and processing of corn and sorghum kernels. The phytase cativity comprises catalysis of phytate (myo-inositol-hexaphosphate) to inositol and inorganic phosphate and is thermotolerant. The nucleic acid is useful in improving the feeding value of phytate rich ingredients or CC as an aid in phytate digestion. The sequence presented is the DNA CC encoding the Escherichia coli appA phytase.
Alignment Scores: Pred. No.:
                                                                             Sequence 1901 BP; 474 A; 499
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                                                                             499 G;
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                                                                                1 Other
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Length: Matches: Conservative:

Percent Similarity:
Best Local Similarity:
Query Match:
DB: 8.17e-195 2182.00 98.1% 98.1% 96.6% Mismatches: Indels:

US-10-601-319-10 (1-432) x ADC87744 (1-1901)

847		788	밁
220	LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu :	201	5
787		728	닭
200	TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys;	, 181	5
727		668	뮍
180	AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis :	, 161	Ş
667	TCCAGTCCCGATCCGTTATTTAATCCTCTAAAAACTGGCGTTTGCCAACTGGATAACGCG	608	dg dg
160		141	Ş
607		548	망
140	AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr	, 121	δ.
547		488	밁
120	GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu	, 101	S
487		428	망
100	GlyHisTyrTrpArgGlnArgLeuValAlalaBpGlyLeuLeuProLysCysGlyCysPro	81	ð
427		368	g
80	ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGluLeuIleAlaTyrLeu	, 61	8
367		308	명
60	ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro	41	S S
307	TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGTCGTCATGGT	248	Дb
40	PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly	, 21	5
247) 188	밁
20	MetLysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAla :	, L	ð

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ADOS0297
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                                                    13-MAY-2004
                                                                                                     US2004091968-A1.
                                                                                                                                                                                                     unsure
                                                                                                                                                                                                                                                                                                                                                       Escherichia coli;
                                                                                                                                                                                                                                                                                                                                                                                                 AppA phytase; bacteria; thermal tolerance; protease stability; foodstuff; phytate; animal feed; fish feed; dough; baking; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli K12 appA phytase DNA.
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                                                                                                                                                                                                /product= "AppA phytase"
401. .403
                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                    note= "Encodes Arg"
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                  Alignment | Pred. No.:
                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for producing phytase that involves CC providing a nucleic acid encoding phytase derived from a bacteria, and CC expressing the nucleic acid in a yeast under conditions that allow CC expression of the enzyme in the yeast. The invention also relates to modified phytase enzyme which has improved thermal tolerance and protease stability at low pH. The phytase enzyme can be used in foodstuffs to commercially at low pH. The phytase enzyme can be used in foodstuffs to commercially at low pH. The phytase enzyme can be used in foodstuffs to commercially animals including mammals, fowls and fishes, commercially significant mammals such as pigs, goats, laboratory rodents, commercially commercially farmed fish such as chicken, ducks, doves, parrot, etc., commercially farmed fish such as guppy, zebrafish, molly, swordtail, composition, higher yields and loading efficiency. The phytase composition, higher yields and loading efficiency. The phytase composition, higher yields and loading efficiency. The phytase composition is Escherichia coli K12 apph phytase DNA.
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01-MAR-1999;
13-APR-1999;
25-MAY-1999;
25-MAY-2000;
24-MAY-2001;
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Mather EJ;
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rrouncing phytase, involves providing nucleic acid derived from bacteria encoding polypeptide having phytase activity, and expressing nucleic acid in yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 7; 74pp; English.
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P-PSDB; ADO50298.
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(ODON/)
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') BARTON N R.

') GARRETT J B.

') O'DONOGHUE E.

') MATHER E J.
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                                                                                                                                                         1901
              ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80
                                                                      ValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpPro
                                                                                                   TCGCTCAGAGTGAGCCGGAGCTGGAAGTGTGGTGGTGATTGTCAGTCGTCATGGT
                                                                                                                              PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly
                                                   GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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; 99US-00259214.
99US-00291931.
; 99US-00318528.
; 2000US-00580515.
; 2001US-00866379.
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Matches:
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ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC

SluAlaArgIleProAlaCysSerLeu 432 	21
ysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420 	01 LeuAl 88 CTGGC
DLysThrProLeuSerLeuAsnThrProProGlyGluValLyst 	81 GlnMe 28 CAGAT
erAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln 380 	61 ArgAr 68 CGTCG
lyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp 360 	41 ThrLe
lyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp 340 	21 Pł 48 Tr
isProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu 320 CCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTG 1147	3-1
luValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300 	28 - Ar
lnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln 280 	େ 61 ନେ ≱
euLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr 260 CTGCAACAAGCACAGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC 967	241 GluIlePheLeuLeuGlı 908 GAGATATTTCTCCTGCA
laAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240 	21 L)
lulysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu 220 	3—£
laPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys 200 	81 J
spAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis 180 	61 As
<pre>spProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160 </pre>	41 Se
laGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr 140 	21 AJ
InValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120 	8 P
YHISTYFTFDATGG1nArgLeuValAlaAspGlYLeuLeuProLygCYsGlYCYsDro 100 ACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGGAAAAAAGGGCTGCCCG 487	28 - ଅ ୧ ଅ

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Search completed: June 14, 2006, 10:58:28 Job time : 581.385 secs

GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlp
-Q-labse/ABSSWEB_gpool/US10601319/runat_12062006_180103_27735/app_query.fasta_1
-Q-labse/ABSSWEB_gpool/US10601319/runat_12062006_180103_27735/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap_-SUFFIX=rnpbm -MINMATCH=0.1
-LOOPEXT=0 -UNITS=blie -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs806p
-USER=US10601319_@CCN_1 1_3524_@runat_12062006_180103_27735 -NCPU=6 -ICPU=3
-NORMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 45 summaries
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Perfect score:
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                                                                      Score Match Length DB
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seq length: 2000000000
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1: EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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5637.400 Million cell updates/sec
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Sequence 1, Appli
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ALIGNMENTS

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Sequence 1, Application US/11056354

| Sequence 1, Application US/11056354
| Publication No. US20050246780A1
| GENERAL INFORMATION:
| APPLICANT: KHORT, Jay M.
| APPLICANT: KRETZ, Keith
| APPLICANT: GRAY, Kevin A.
| APPLICANT: GRAY, Kevin A.
| APPLICANT: GARRETT, James B.
| APPLICANT: GARRETT, James B.
| APPLICANT: MATHUR, Eric J.
| TITLE OF INVENTION: FPYTASES, NUCLEIC ACIDS ENCODING THEM APPLICANT: MATHUR, Eric J.
| TITLE OF INVENTION: FOR MAKING AND USING THEM FILE REFERENCE: 564462001803/D1370-9C1
| CURRENT FILING DATE: 2005-02-11
| PRIOR APPLICATION NUMBER: US/11/056,354
| PRIOR APPLICATION NUMBER: US 10/156,660
| PRIOR FILING DATE: 2001-05-24
| PRIOR APPLICATION NUMBER: US 09/866,379
| PRIOR PILING DATE: 2001-05-24
| PRIOR APPLICATION NUMBER: US 09/866,379
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  661
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CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
                                                                                                                             AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                                                      LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
                                                                                   TATCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
                                                                                                TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
                                                                                                                                                                                   SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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Sequence 1, Application US/1015660
Publication No. US20030103958A1
GENERAL INFORMATION:
APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: O'Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENGITTILE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENGITTILE OF INVENTION: AND METHODS FOR MAKING ANI
FILE REFERENCE: 09010-029007
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: 2001-05-24
PRIOR FILING DATE: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 08/910,798
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OTHER INFORMATION: modified phytase
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AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
                                        GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                                                                                                                                                                   Sequence 9, Application US/10601319

Publication No. US20040091968A1

GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith A.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Grey, Kevin A.

I APPLICANT: O' Donoghue, Eileen

APPLICANT: To Donoghue, Eileen

APPLICANT: Nathur, Eric J.

ITILE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF INTILE OF INVENTION: AND USING THEM

FILE REFERENCE: 09010-029011

CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/86,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

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US-10-601-319-9
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SEQ ID NO 9
                                                         TYPE: DNA ORGANISM: Artificial Sequence
                 FEATURE:
OTHER INFORMATION: modified phytase
                                                                                               LENGTH: 1308
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Best Local Similarity:
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LOCATION: (1)...(1296)
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            ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
                                                        AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
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 CGCACGCCAGAGGTTGCCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
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FILE DOE INVENTION:
FILE TEFERENCE: 56446201822
CURRENT FILING DATE: 2004-09-01
FRIOR APPLICATION NUMBER: US/09/866,379
FRIOR FILING DATE: 2001-05-24
FRIOR FILING DATE: 2001-05-24
FRIOR FILING DATE: 2000-05-25
FRIOR APPLICATION NUMBER: US 09/580,515
FRIOR APPLICATION NUMBER: US 09/318,528
FRIOR APPLICATION NUMBER: US 09/318,528
FRIOR FILING DATE: 1999-05-25
FRIOR FILING DATE: 1999-04-13
FRIOR FILING DATE: 1999-04-13
FRIOR APPLICATION NUMBER: US 09/259,214
FRIOR APPLICATION NUMBER: US 09/259,214
FRIOR APPLICATION NUMBER: US 08/910,798
FRIOR APPLICATION NUMBER: US 08/910,798
FRIOR APPLICATION NUMBER: US 08/910,798
FRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-10-933-115-9
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 Alignment Scores: Pred. No.:
                                                        US-10-933-115-9
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Rc
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eile
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Publication No. US20050281792A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
TITLE OF INVENTION: THEREOF
                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                            NAME/KEY: CDS
LOCATION: (1)
                                                                                                                 FEATURE:
                                                                                                                                 OTHER INFORMATION: modified phytase
                                                                                                                                                                                        TYPE: DNA
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Score:
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                                                               LeuThrProHisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeu
                                                                                                                                                                                                                                                                                   GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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                                          TTGACGCCCCATCCACCGCAAAAAACAGGCGTATGGTGACATTACCCACTTCAGTGCTG
                                                                                                                     CGCACGCCAGAGGTTGCCCGCAGCCGCGCCACCCCGTTATTAGATTTGATCAAGACAGCG
                                                                                                                                                 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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  PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
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Publication No. US20040091968A1

GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Gray, Kevin A.

APPLICANT: Gray, Kevin A.

APPLICANT: Barton, Nelson Robert

APPLICANT: Barton, Nelson Robert

APPLICANT: Mathur, Efic J.

TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING

TITLE OF INVENTION NUMBER: US/10/601,319

CURRENT PAPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 1999-05-25

PRIOR PILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                       Score:
                                                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                                                   ; FEATURE:
, NAME/KEY: misc feature
; LOCATION: 403 -
; OTHER INFORMATION: n =
US-10-601-319-6
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GENERAL INFORMATION:
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
APPLICANT: Barton, Nelson Robert
APPLICANT: Garyett, James B.
APPLICANT: Garyett, James B.
APPLICANT: Mathur, Eric J.
APPLICANT: Mathur, Eric J.
APPLICANT: Mathur, Eric J.
CURRENT ENVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US(10/601,319
CURRENT APPLICATION NUMBER: US 09/866,379
PRIOR APPLICATION NUMBER: US 09/86,515
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
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PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1901
FEATURE:
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US-10-933-115-5

(Sequence 5, Application US/10933115

Pablication No. US20050281792A1

(ENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith A.

APPLICANT: Barton, Nelson Robert

APPLICANT: Garay, Kevin A.

APPLICANT: Garay, Kevin A.

APPLICANT: Garay, Kevin A.

APPLICANT: Mathur, Exic J.

APPLICANT: Mathur, Exic J.

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 564462001822

CURRENT APPLICATION NUMBER: US/10/933,115

CURRENT APPLICATION NUMBER: US/9/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR PILING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR PILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR PILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR PILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 1901

TYPE: NUMA
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; OTHER INFORMATION: n =
US-10-933-115-5
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Best Local Similarity:
Query Match:
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TYPE: DNA
ORGANISM: Escherichia
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ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu 80
                                 GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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Matches:
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IleValAsnGluAlaArgIleProAlaCysSerLeu
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                                                               LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
                                                                                                                        GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
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TITIE OF INLENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELLITAA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/210,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2000-10-2-09
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR FILING DATE: 2000-10-2-09
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-10-2-16
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-10-2-16
PRIOR APPLICATION NUMBER: 60/257,931
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US-10-282-122A-7167
Sequence 7167, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Escherichia
US-10-282-122A-7167
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Yamamoto, Robert
Forsyth, R.
Xu, H.
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Zyskind, Judith
Wall, Daniel
Trawick, John
TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGGAAAGTGTGGTGATTGTCAGTCGTCATGGT
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Malone, Cheryl
Haselbeck, Robert
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                                                                            GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                                                                                                                                                                             ThrLeuProGlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrp
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                                                                                                                            CGTCGGCTAAGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAG
                                                                                                                                              ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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Sequence 7. Application US/09866379

Patent No. US20020136754A1

GENERAL INFORMATION:

APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: O'DONOGHUE, Bileen
ITITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/31,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

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PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

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Best Local Similarity:
Query Match:
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NAME/KEY: misc feature
; LOCATION: (1). (1901)
; OTHER INFORMATION: n is any nucleotide
US-09-866-379-7
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US-09-866-379-7
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SEQ ID NO 7
LENGTH: 1901
TYPE: DNA
ORGANISM: Escherichia coli
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GlnSerGlyGlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGlu 120
                                                                                                                                                          ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGlyGluLeuIleAlaTyrLeu
                                                                                                                                                                                                            GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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                                         GGACATTACCAACGCCAGCGTCTGGTAGCCGACGGATTGCTGGCGAAAAAAGGGCTGCCCG
                                                                  GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                                                                                                           ACCTGGCCGGTAAAACTGGGTTGGCTGACACCGCGNGGTGGTGAGCTAATCGCCTATCTC
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RESULT 10
US-09-866-379-9
; Sequence 9, Application US/09866379
; Patent No. US20020136754A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1901)
; OTHER INFORMATION: n is any
US-09-866-379-9
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FILE REFERENCE: DIVERI370.7

CURRENT PILING DATE: 2001-05-24

CURRENT PILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR PILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1997-08-13

NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 9

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APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: BARTON, Nelson
APPLICANT: O'DONGSHUE, Bileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES
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   SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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US-10-156-660-3

Sequence 3, Application US/10156660

Publication No. US20030103958A1

GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Short, Jay M.

APPLICANT: Gray, Keith

APPLICANT: Garrett, James B.

APPLICANT: Garrett, James B.

APPLICANT: O'Donoghue, Eileen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM

FILE REFERENCE: 09010-029007

CURRENT APPLICATION NUMBER: US/10/156,660
                                                                                                                                                                                                                                                                                                  IleValAsnGluAlaArgIleProAlaCysSerLeu 432
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SEQ ID NO 3
LENGTH: 1901
TYPB: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
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PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR PLING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/292,214
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-13
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GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Stort, Jay M.

APPLICANT: Kretz, Keith A.

APPLICANT: Gray, Kevin A.

APPLICANT: Barton, Nelson Robert

APPLICANT: Garrett, James B.

APPLICANT: O' Donoghue, Eileen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: RECOMBINANT PHYTASES AND

TITLE OF INVENTION: AND USING THEM

FILE REFERENCE: 0910-029011

CURRENT APPLICATION NUMBER: US/10/601,319

CURRENT FILING DATE: 2003-06-20
                                                                                                                                                                                                                                                                                                                RESULT 12
US-10-601-319-7
                                                                                                                                                                                                                                                                            Sequence 7, Application US/10601319 Publication No. US20040091968A1
PRIOR APPLICATION NUMBER: US 09/866,379 PRIOR FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: US 09/580,515
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PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 7
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LOCATION: 403
OTHER INFORMATION: n = A,T,C
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Best Local Similarity:
Query Match:
DB:
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LOCATION: (188)...(1483)
FEATURE:
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ORGANISM: Escherichia coli
FEATURE:
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 TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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Matches:
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US-10-933-115-7

(Sequence 7, Application US/10933115

Publication No. US20050281792A1

(GENERAL INFORMATION:

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Kaith A.

APPLICANT: Gray, Kevin A.

APPLICANT: Garrett, James B.

APPLICANT: Mathur, Eileen

APPLICANT: Mathur, Eileen

APPLICANT: Monoghue, Bileen

APPLICANT: Motor THEREOP

FITLE OF INVENTION: THEREOP

FILE REFERENCE: 554462001822

CURRENT APPLICATION NUMBER: US/10/933,115

CURRENT FILING DATE: 2004-09-01

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US/09/866,379

PRIOR APPLICATION NUMBER: US/09/515

PRIOR APPLICATION NUMBER: US/09/580,515

PRIOR APPLICATION NUMBER: US/09/580,515

PRIOR APPLICATION NUMBER: US/09/318,528

PRIOR APPLICATION NUMBER: US/09/318,528

PRIOR APPLICATION NUMBER: US/09/318,528

PRIOR PILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US/09/291,931
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APPLICANT: SHORT, Jay M.

APPLICANT: GRAY, Kevin A.

APPLICANT: GRAY, Kevin A.

APPLICANT: BARTON, Nelson R.

APPLICANT: BARTON, Nelson R.

APPLICANT: GARRETT, James B.

APPLICANT: MATHUR, Eric J.

TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEN

TITLE OF INVENTION: FOR MAKING AND USING THEM

FILE REFERENCE: 564462001803/D1370-9C1

CURRENT APPLICATION NUMBER: US/11/056,354

CURRENT FILING DATE: 2005-02-11

PRIOR APPLICATION NUMBER: US 10/156,660

PRIOR FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-05-25

PRIOR FILING DATE: 1999-04-13

PRIOR PILING DATE: 1999-04-13

PRIOR APPLICATION NUMBER: US 09/259,214
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                                      LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240
                                                                                                                                                                                                    AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
                                                                                                                                                                                                                                                                                                GCCTTCGCCGCGCGCGCACCTGACTGTGCAATAACCGTACATACCCAGGCAGATACG
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                                                                                                                                                                                                                                                                                                                                                      CAGTCTGGTCAGGTCGCGATTATTGCTGATGTCGACGAGCGTACCCGTAAAACAGGCGAA
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                     AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
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Matches:
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607 140 120

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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUB, Eilsen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHY
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US 09/880,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-04-13
PRIOR PRILING DATE: 1999-08-13
NUMBER OF ESG ID NOS: 10
SOCTWARE: PatentIn version 3.1
SEQ ID NOS: 10
TENTYTH: 1901
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     TYPE: DNA
ORGANISM: Escherichia
FEATURE:
                                             LENGTH: 1901
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Query Match:
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; LOCATION: (1). (1901)
; OTHER INFORMATION: n is
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ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300
                                                                                                              GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                                                                                                 LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr
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                                                                                              GAGATATTTCTCCTGCAACAAGCACAGGGAATGCCGGAGCCGGGGTGGGGAAGGATCACC
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		TTACGCAA	heThrGln			CTTTACAG	hrLeuGln	AACGCTGG	luArgTrp	TCAACTGG	euAsnTrp	CAGTGCTG		AGACAGCG
		1447	420	1387	400	1327	380	1267	360	1207	340	1147	320	1087

Search completed: June 14, 2006, 15:10:36 Job time: 1441.42 secs

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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US01_NEW_PUB.seq:*
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; Sequence 848, Application US/10505928

publication No. US20060088532A1

; GENERAL IMFORMATION:

i APPLICANT: Ludwig Institute for Cancer Research et

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR PILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866
              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                       Score:
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                                                                                       Pred. No.:
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SEQ ID NO 848
LENGTH: 2661
TYPE: DNA
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ORGANISM: Homo
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                                               ProProGlnLysGln-----AlaTyrGlyValThrLeuProThrSer------
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Sequence 14217, Application US/10449902

| Publication No. US20060123505A1
| GENERAL INFORMATION: APPLICANT: National Institute of Agrobiological Sciences. APPLICANT: Bio-oriented Technology Research Advancement Institution APPLICANT: The Institute of Physical and Chemical Research. APPLICANT: Poundation for Advancement of International Science. APPLICANT: Poundation for Advancement of International Science. ITITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US CURRENT APPLICATION NUMBER: US/10/449,902
| CURRENT APPLICATION NUMBER: US/202-203269
| PRIOR APPLICATION NUMBER: JP 2002-203269
| PRIOR FILING DATE: 2002-05-30
| PRIOR FILING DATE: 2002-12-11
| NUMBER OF SEQ ID NOS: 56791
| SOPTWARE: Patentin Ver. 2.1
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                                                                                                                                                               US-10-601-319-10 (1-432) x US-10-449-902-14217 (1-1482)
                                                                                                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: OTYZA BALIYA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK064835
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1482
TYPE: DNA
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AGCTCGTCCTCGGTGGCGTCCACGCACACGCCGTTGATGTCGCCAGATCTCCCCCT---
                              HisGlyValArgAlaProThrLysAlaThrGlnLeuMetGlnAspValThr-ProAspAl
                                                                             TCGATCTTCACCTTCTCCCGCCCCACGGTCAGCTTCCCTTCGTTGGTGAGCCGGAAC
                                                                                                        SerAlaPheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArg
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
FRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-363870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-449-902-9793/c
                                                                                                                                                                                                                                                  Sequence 9793, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
      SEQ
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK107141;
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9793
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Best Local Similari
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ORGANISM: Oryza sativa
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GCAGGCGCCCTGGGGCCTCCAGGGTTCTCATCTCTGCGACCAAAGTGGACGCGCTGAC
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|||:::
                                                       ----ThrGlnAlaLeuProSerGluLeuLysValSerAlaAspCysVal----SerLeuTh
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                                                                                                                 ATCGAGCAGGAGCATCACGATGÀÀGTCGTCGGÀGGCGAGGCCGGGGGGGGGCGCTCGCTGTA
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Best Local Similarity:
                                                                                                                                                                                                                                                                 Score:
                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 21879
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APPLICANT: Bio-oriented Technology Research Advancement Institut
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK072104
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1470
TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                No.:
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tGlnAspValThr-ProAspAlaTrpProThrTrpProValLysLeuGly-------
                                                                        SerValVal-IleValSerArgHisGlyValArgAlaProThrLysAlaThrGlnLeuMe 51
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                                         APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1

SOFTWARE: Patentin Ver. 2.1
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   ORGANISM: Oryza sativa
                 LENGTH: 2822
TYPE: DNA
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156 GlnLeuAsp-----AsnAlaAsnValThrAspAlaIleLeuGluArgAlaGlyGlySer 173
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100 ---GGTGGCCÁGGGGGAGGAGGACCÁGGCGGTGGÁGAGGTGCGAGCACGACÁTGGCTGG
                                                            GlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrp
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                                                                                                                              GCCGCAGCTAGGAGCGGAGCGGCGGCG-
                                                                                                                                                                                          CysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeu
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DATABASE ACCESSION NUMBER: AK105071
DATABASE ENTRY DATE: 2002-08-28
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                                                                                                                                                 CACCAGCTTCATCGCCTC------CGTGATCTTCTGCGTGTTGCGCACCGA
                                                                                                                                                                                                                                 IleAlaAspPheThrGlyHisTyrGlnThrAlaPheArg-------
                                                                                             GTCGATGCGGCTCCGCAGCTCACGCAGCAGCACCACCTGCAGGCGGCCGCTGCT
                                                                                                                      GlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAsp
                                                                                                                                                                                                                                                                                    GlnLeuAsp-----AsnAlaAsnValThrAspAlaIleLeuGluArgAlaGlyGlySer 173
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|-----cagetecaeggtagetrecettegttggtgagetggaa-----eag
                                                                 CysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeu
                                                                                                                                                                          ---GluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLys
                                                                                                                                                                                                      GAGGTCGATGTCCTCCGTCTGGATCTCCTGGTTCATGTTGTAGAGCACCTCCACCAGCGC 1758
                                                                                                                                                                                                                                                                                                               GCGCTCGCCGGTGAGGACGACGACGCGACCTTCTTGACGGGGCGGATGCGGGTGAGGGG 1818
                                                                                                                                                                                                                                                                                                                                        AspThrSerSerProAsp------ProLeuPheAsnProLeuLysThrGlyValCys 155
                                                                                                                                                                                                                                                                                                                                                                                                                      GTAGGCGTTGCCCTACCGACGCTGACGACGGTGTACTCGAGGCCGAGCTGCTTGAG
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; ORGANISM: Homo
US-11-189-279-64
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US-11-189-279-64
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Publication No. US20060115829A1
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APPLICANT: LIUO, WANG
TITLE OP INVENTION: A METHOD OF TREATING CANCER
FILE REFERENCE: UTXC:875US
CURRENT APPLICATION NUMBER: US/11/189,279
CURRENT FILING DATE: 2005-07-26
PRIOR APPLICATION NUMBER: 60/598,554
PRIOR FILING DATE: 2004-08-03
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                                         uAlaSerMetLeuThrGluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGl
                                                                                                                           aLeuProSerGluLeuLysValSerAlaAspCysValSerLeuThrGlyAlaValSerLe 235
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                                                                                    CTTACCTTCCATTCTTAGCCTAACTCCCGTGTGC
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                                                                                                                                                                                                                                                                                                         aAspPheThrGlyHisTyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPhePr 195
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US-11-284-978-14
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                                                                   US-10-601-319-10 (1-432) x US-11-284-978-14 (1-1221)
                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/284,978
CURRENT FILING DATE: 2005-11-22
PRIOR APPLICATION NUMBER: US 60/633,008
PRIOR FILING DATE: 2004-12-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Garrett-Engele, Philip W.
APPLICANT: Raymond, Christopher K.
TITLE OF INVENTION: ALTERNATIVELY SPLICED ISOFORMS OF
TITLE OF INVENTION: PURINERGIC RECEPTOR P2X, LIGAND-GATED ION CHANNEL,
TITLE OF INVENTION: 3 AND 4 (PZRX3, PZRX4)
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: RS0222
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TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                              No.:
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 GGAGAAAGTGGAAĠĊĠGAGAAAĠĀĊĊTĀACAAGTTGTAAGACTGCGCTGCCCTTGGGCCC 23592
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                             FILE REFERENCE: 022041-002020US
CURRENT APPLICATION NUMBER: US/11/145,307A
CURRENT FILING DATE: 2005-06-03
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PRIOR PILING DATE: 2004-06-04
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                                                                                                                                                                                                                                                             Sequence 189, Application US/11145307A Publication No. US20060094035A1 GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Arcturus Bioscience,
APPLICANT: Erlander, Mark G.
APPLICANT: Ma, Xiao-Jun
                                                                                                                                                                                           TITLE OF INVENTION: Identification of Tumors
ORGANISM: Homo sapiens
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rLeuGly GTTA	sLeuGly ACTCAAA	aThrGln AACC	uLeuLys A	oPheLeu CTGACAC	01-834-1		TRAAGCAGGAA CCGCCCTTTG YTG1YValThr TTCGCTCCGGG TTCACGGCTCCGGG TTCACGGCCAG TTCACGGCCAG TTCACCGCACATC CACCCCACATC CACCCCACATC CACCCCACATC SUS/10/501,8 T/US03/0203 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Ξ
LeuIleAlaTyrLeuGlyHisTyrTrpArgGlnArgLeuValAlaAspGly ::: 	ThtTtpProVallysLeuGlyGluLeuThrProArgGlyGlyGlu 	LeuMet	PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHi :: TTCAGGGAGAAGGAAGCTCCA	Q-H	-1	Length: Matches: Conservat Mismatche Indels: Gaps:	TCACTCACCCTTGGCCATAAAGCNGAAAACCCCCAGGGTGTCCAGTCTAGCTCCACCCCO	=
TrpArgG	ThrProa : :AAGTAA	31nAspv	Servalv	LeuLeuIleP ::: CTGGTTAGCC	12225)	ive:	CGAGGTGTC UITELYSTH CG G GG GCCCTTCAA GCCCTTCAG CCTCTCAGG CG1yG1yG1	=
lnArgLe GCAACCC	rgGlyGl :: aaggacc	alThrPz	alīleva	roLeuTh CATTGAC		12225 109 54 167 167 139	ThralaLe ThralLe ThralaLe Thra	:
ArgGlnArgLeuValAlaAspGly 	yGlu ccacacac		lSerAr	ProLeuThrProGlnS CCATTGACCAGGACTG			LeuThrPr Phe TTTCCCCA TTTCCCCA GAGATGGT 4 09 08	=
aaspGly agtaagt	TCAACC	aTrpPro	gHisGly GGC	rProGlnSerAla CAGGACTGTGACG			roHisPr ATGCTGC euAsnTr : TGGGGCC TGGGGCC	<u>:</u> =
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3894 TGCCGCTTCATACATGAAGGTGAAGCCTTTCCCCC------
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                                                                                                                                                                                                                                                                                  uLeuValPheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLe 374
                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGATGTGGAGATCAACCCCTTGTGAGTGAATGCTGACCCCATTGATAGAGAC-GGAAA 3521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAl 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluArgAlaGlyGlySerIleAlaAgpPheThrGlyHis-----TyrGlnThrAla 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluArgThrArgLysThrGlyGluAlaPheAlaAlaGlyLeuAlaProAspCysAlaIle 132
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                                                                                                                                                                                                                                  ACTGTGTGTGAACCGGAGCCAAGGCATCCTGGACGTGGACTTCCACATCCAAATCCGTAT 3407
                                                                                                                                                                                                                                                                                                                                       TTCTGTGGAGACCAGCTGGCAGTGG---GGGCAGTGCCACCTCCAGGCCCCA---AGCCG 3467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLe 244
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                          CTGCTATATTGCTTATGTTTCTGCTCAGAGTCACAATAACTGGATTTAAGGAAGAGACAT 3305
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                                                                       ----GluValLysLeuThrLeuAlaGlyCysGluGluArg---- 407
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    CCTCGCCÁCTCCÁATGACCAGGGTCTCACCGC

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APPLICANT: MOSTIS, MCDOMAID

APPLICANT: ROSENBERGY, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117
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; ORGANISM: Homo
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Fry, Kirk
Woodward, Robert
Ly, Ngoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaGlnSerGluPro---GluLeuLysLeu------GluSerValValIleValSer 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAlaIleLeuIleProPheLeuSerLeuLeuIleProLeuThrProGlnSerAlaPhe 21
ATCTCAGGACTCCAGCCTGGCAACTCCTACTGGCTGCAGCTGCGCAGCCGAACCTGATGGG
                                             IleAlaTyrLeu-----GlyHisTyrTrpArgGln---ArgLeuValAlaAspGly 92
                                                                                                                                                                                                       GCCTCTGCTCTGGACCAGTCTCCATGTGCTCAGCCCACAATGCCCTGGCAAGATGGACCA
                                                                                                                                                                                                                                                                                                               GGTGGGAGCCAGCCAGGGAACTTCAGATCAGCTGGGAGGAGCCAGCTCCAGAAATCAGT
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AspLysThrProLeuSerLeuAsnThrProProGlyGluVal----------
                                                                                 SerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArg
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                                                                                                                                 CGGGTCCTAGGCCAGTACCTTAGGGACACTGCAGCCCTGAGCCCCCCAAGGCCACAGTC
                                                                                                                                                                                                                       TTTCCTGCACACTACAGGAGACTGAGGCATGCCCTGTGGCCCTCACTTCCAGACCTGCAC 1653
                                                                                                                                                                                                                                                                                                             CTCTGCATCTAGTGCTGGGCCTCAGCGCCGTCCTG-GGCCTGCTGCTGAGGTGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuPheIleAlaGly-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThr 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H1s-----GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeu 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuGlnGlnAlaGlnGlyMetProGluProGly-----TrpGlyArgIleThrAspSer 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGTGACCACAGCCCCGGGTACTGTTCAC----AGCTACCTGGGCTCCCCTTTCTGG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeu 244
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                                            TCAGATACCTGTGAAGAAGTGGAACCCAGCCTCCTT---GAAATCCTCCCCAAGTCCTCA 1770
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
FRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 315
LENGTH: 2408
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Best Local Similarity:
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US-11-293-697-315
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ORGANISM: Homo
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                                        124 AlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThrSerSerPro 143
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                                                                                                                                                                                                                      84 TrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysProGlnSerGly 103
                                                                                                                                                                                                                                                                                                                                                                                                   61 ThrTrpProValLysLeuGlyGluLeuThrProArgGly------GlyGluLeuIleAla 78
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GCAGGCGCAGGACCC---
                                                                                                                                                                                  ACCAGAAAACGAAGAACGCCCGGAGGCGGGAGGCCGGAGGCAGGCTGC---
                                                                                                                                                                                                                                                                                                                                                                  GTTTGGCTTTTGTCCCGCGCCGAGGTCCGGCCCAGGAGTGCGCTTGGGAGCTCCCGGCGC 461
                                                                                                                               GlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGluAlaPheAla 123
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                                                                                         -----TGGCTGGAGAACCGACGGCAACGACGGCGCAAAGCCGGC--
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----ACCCTGACGCCGCCTCTCCCAGCCGGCTCTCCT
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9 LeuserLeulleProLeuThrProGln	Alignment Scores: Pred. No.: 98.50 Score: 98.50 Matches: 93 Percent Similarity: 24.3* Conservative: 93 Best Local Similarity: 4.4* Cusservative: 103 Cuery Match: 103 Cuery Match: 103 Cuery Match: 103 Cuery Match: 103 Cuery Match: 103 Cuery Match: 104 Cuery Match: 105 Cuery Match: 106 Cuery Match: 107 Cuery Match: 108 Cuery Match: 109 Cuery Matches: 109 Cue	NGTH: PE: DN GANISM ATURB: HER IN HER IN 857-26		Cy 255 GJYTP 256 Db 867 GCCTGG 872 RESULT 12 US-10-857-260-27 ; Sequence 27, Application US/10857260 ; Publication No. US20060110742A1	215 AlaLeurro 	144 AspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAlaAsn
Qy 295AspLeuIleLysThrAlaLeuThrProHisProProGlnLysGlnAlaTyrGlyV 313		Qy 230 hrGlyAlaValSerLeuAlaSerMetLeuThrGlu	Qy 178ThrGlyHisTyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPh 194	Qy 141 rSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAlaAs 161 :::	Qy 104GlnValAlaIleIleAlaAspValAspGluArgThrArgLysThrGlyGluAla 121	Qy 45 ThrLysAlaThrGlnLeuMetGlnAspValThrProAspAlaTrpProThrTrpProVal 64

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Best Local Similarity:
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; ORGANISM: Homo sapiens
US-11-317-329-2
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 2696
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APPLICANT: Inohara, Naohiro
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
CURRENT FILING DATE: 2005-12-22
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192 LeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSer 211
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                                                              TGGACCCCTCTTCACCTGGCTGCA-----
                                                                                                                                          ACTGCGCGCCTGCTCCTGGACCACGGGGCCTGTGTGGATGCC---CAGGAACGTGAAGGG
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                                                                                                                                                                                                                                                                                                        GCCCAGGACCAGCAACCCGACCTCTGTGCCCTGCTTTTGGCACATGGTGCTGATGCCAAC 1641
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                                                                                                GlySerIleAlaAspPheThrGlyHisTyrGlnThrAlaPheArgGluLeuGluArgVal 191
                                                                                                                                                                                                                          CGAGTGGATGAGGATGGCTGGGCCCCACTGCACTTTGCAGCCCAGAATGGGGATGACCGC 1701
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                                                                                                                                                                                                                                                                                                                                             ---AspCysAlaIleThrValHisThrGlnAlaAspThrSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGTGAGGTTGCTGCTGGCCCACGAGGTAGACGTGGAC 1542
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Alignment Scores
Pred. No.:
                                                              ; ORGANISM: H
US-11-317-329-4
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                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2696
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/11317329
Publication No. US20060105413A1
GENERAL INFORMATION:
                                                                                                                                                                                               APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Nachiro
TITLE OF INVENTION: Methods and Compositions
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/11/317,329
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION NUMBER: US/10/128,174
PRIOR FILING DATE: 2002-04-23
                                                                                                                                                                                PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
                                                                                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATCCAACACCTGCTGAAGAGTGGGAGCGGTCCCTGATGCCCTTGACCAGAGCGGCTAT
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Qy 192 LeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSer 211	SCOTE: SINILARITY: 23.1k Percent Similarity: 21.9k Percent Similarity:
Alignment Scores: Pred. No.: 96.50 Score: 96.50 Matches: 104 Score: Percent Similarity: 13.1% Best Local Similarity: 12.1.9% Mismatches: 167 Query Match: 7 Gaps: 22 US-10-601-319-10 (1-432) x US-11-317-329-5 (1-2696) Qy 8 PheLeuSerLeuLeuIleProLeuThrProGlnSerAlaPheAlaGlnSerGlu 25	Db 1999 CCCATCCAACACCTGCTGAAGAGTGGAGCGGTCCCTGACCAGGCGGTAT 2058 Oy 312 Gly

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2364CCACCTGGCGTCCAGAGGAGCACCTTCCTGAGTGTCATCAA 2405	392 ThrProProGlyGluValLysLeuThrLeuAlaGlyCysGluGlu 406	2316 GTGTGGGGCTGACCCCAATGCTGCAGAGCAGTCAGGCTGGACACCCCT 2363	375 ValPheGlnThrLeuGlnGlnMetArgAspLysThrProLeuSerLeuAsn 391	2292	355 LeuValPheGluArgTrpArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeu 374

Search completed: June 14, 2006, 14:25:58 Job time: 98.6927 secs

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Result
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-Q-/abss/ABSSWEB spool/US10601319/runat_12062006 180052 27516/app_query.fasta_1
-DB=SST -QFMT=fastap -SUFFIX=rst -NINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.dd1 -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10601319_@CGN 1 1 12067 @runat 12062006 180052 27516 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Perfect score:
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ALIGNMENTS

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DEFINITION

PRIO142b B11 - PRIO142b.B21 (853) Mixed stage fosmid library of P.

BRIO142b B11 - PRIO142b.B21 (853) Mixed stage fosmid library of P.

BRIO16B VAR. California Pristionchus pacificus genomic, genomic

CLG62734

VERSION

CLG62734

VERSION

CLG62734.1 GI:50150877

KEYMORDS

SOURCE

ORGANISM

Pristionchus pacificus

Bukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

REFERENCE

1 (bases 1 to 853)

AUTHORS

Sinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

PUBMED

JOURNAL

PUBMED

COMMENT

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Pax: 00497071601498

Email: ralf. sommer&tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

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Class: fosmid
                                                     BJ074127
616 bp mRNA linear EST 29-SEP-2003
BJ074127 NIBB Mochii normalized Xenopus tailbud library Xenopus
laevis CDNA clone XL090j06 5', mRNA sequence.
Xenopus laevis (African clawed Xenopus laevis
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var. California"
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/mol_type="genomic DNA"
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The information of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL090]06"
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1001.00
96.6%
96.6%
44.3%
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Indels:
Gaps:
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Matches:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 616)

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
```

Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, (1918) 81-559-81-6855
Fax: 81-559-81-6855 is available through the following

/tissue type="whole embryo" /dev_stāge="stage 25" /clone_lib="NIBB Mochii normalized Xenopus tailbud

Conservative: 0070

109 AlaAspValAspGluArgThrArgLysThrGlyGluAlaPheAlaAlaGlyLeuAlaPro 128 249 GlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHisGlnTrpAsnThrLeu 268 ValalaaspGlyLeuLeuProLysCysGlyCysProGlnSerGlyGlnValAlaIleIle 108 AspCysAlaIleThrValHisThrGlnAlaAspThrSerSerProAspProLeuPheAsn GTAGCCGACGGATTGCTGGCGAAAAAGGGCTGCCCGCAGTCTGGTCAGGTCGCGATTATT GAACGGGTGCTTAATTTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAACAGGACGAA ArgAlaGlyGlySerIleAlaAspPheThrGlyHisTyrGlnThrAlaPheArgGluLeu 188 GACTGTGCAATAACCGTACATACCCAGGCAGATACGTCCAGTCCCGATCCGTTATTTAAT GCTGATGTCGACGAGCGTACCCCGTAAAACAGGCGAAGCCTTCGCCGCCGGGCTGGCACCT TTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTTCTCCTGCAACAAGCA LeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePheLeuLeuGlnGlnAla 248 SerCysSerLeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspCysValSer AGGGCAGGAGGGTCAATTGCTGACTTTACCGGGCATCGGCAAACGGCGTTTCGCGAACTG ProLeuLysThrGlyValCysGlnLeuAspAsnAlaAsnValThrAspAlaIleLeuGlu 168 AGCTGTTCATTAACGCAGGCATTACCATCGGAACTCAAGGTGAGCGCCGACAATGTCTCA 148 196 316 436 496 556 136 228 256 208

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RESULT 3
BU713770
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AUTHORS
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ORGANISM
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Schistosoma japonicum
Schistosoma japonicum
Bukaryota, Metazoa, Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 529)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
McManus,D.P., Xue,C.L., Peng,Z., Chen,Z. and Han,Z.G.
Evolutionary and blomedical implications of a Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BU713770 529 bp mRNA linear BST 23-OCT-2003 SJAABUGG2 Adult SJC 7/94 Schistosoma japonicum cDNA similar to pdb|1DKP|A Chain A, Crystal Structure Of Phytate Complex Of Escherichia Coli Phytase At Ph 6.6. Phytate Is Bound With Its 3-Phosphate In The Active Site. Hg2+ Cation Acts As An Intermolecular Bridge, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zeguang Han Chinese National Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complementary DNA resource Nat. Genet. 35 (2), 139-147 (2003)
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BU713770.1 GI:28321126
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/ tissue type="Mhole body"
//tissue type="Whole body"
//lab_host="Mouse and rabbit"
//lab_host="Mouse and rabbit"
//clone lib="Adult SJC 7/94"
//clone lib="Adult SJC 7/94"
//clone lib="Adult SJC 7/94"
//note="Vector: Lambda ZAP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Erisbane, Australia (GIMR), and stoored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
GIMR from lysates of these worms by oilgo dT
chromatography, using a kit from pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oilgo-dT-Xhol-primer and synthesis was
primed with an oilgo-dT-Xhol-primer and synthesis was
primed with an oilgo-dT-Xhol-primer and synthesis was
accomplished with RNAse H and T4 DNA polymerase. The
double stranded cDNA was ligsted to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Schistosoma japonicum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="Chinese (Anhui) strain"
/db_xref="taxon:6182"
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clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."

ACCESSION VERSION KEYWORDS RESULT 4 CA093060 LOCUS REFERENCE SOURCE DEFINITION US-10-601-319-10 (1-432) x BU713770 Query Match: Best Local Similarity: Score: Percent Similarity: Alignment ORGANISM 481 384 421 364 361 344 301 324 241 304 181 121 264 244 LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 224 AlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe 61 Vettore,A.L., da Silva,F.R., Kemper,E. The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 (2001) Saccharum officinarum Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum Saccharum officinarum CA093060.1 GI:34946367 CA093060 3', mRNA sequence. SCCCCL2001D10.b CA093060 complex. GlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuPro GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrPro GATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGTGAAACTG GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu GluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAlaLeuThrPro GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT AspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeu AGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAGCAGATGCGT SerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArg GGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGGCGTCGGCTA CATCCACCGCAAAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCC HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla (bases 1 to 746) 3.12e-81 905.00 98.9% 98.9% 746 bp mRNA linear EST 23-SEP-2003 CL2 Saccharum officinarum cDNA clone SCCCCL2001D10 (1-529)Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: Kemper, E.L. and Arruda, P 174 0 0 Saccharum officinarum 528 480 383 420 363 360 343 300 323 240 303 180 283 263 60 243 120

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  344
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Centro de Biología Molecular e Engenharia Genetica
Centro de Biología Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
                                                              GlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrpThrLeuPro 343
                                                                                                                                         HisProProGlnLysGlnAlaTyrGlyValThrLeuProThrSerValLeuPheIleAla 323
                                                                                                                                                                                                                  GluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAlaLeuThrPro 303
                                                                                                                                                                                                                                                                                            GlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGlnProAspAsnThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeu 363
                                                                                                                                                                                                                                                                                                                                                                           LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis
                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATATTT
                                                                                                                 CATCCACCGCANAAACAGGCGTATGGTGTGACATTACCCACTTCAGTGCTGTTTATCGCC
                                                                                                                                                                                             GAGGTTGCCCGCAGCCGCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCC
                                                                                                                                                                                                                                                                        CTCCTGCAACAAGCACAGGGAATGCCGGGAGCCGGGGTGGGGAAGGATCACCGATTCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib=CCL?"
/clone lib=CCL?"
/note="Organ: Pool of sugarcane calli submitted to low
/note="Organ: Pool of sugarcane calli submitted to low
(4oC) and high (37 C) temperature stress; Vector:
pBlurScript; Site 1: EcoRI; Site 2: XhoI; An
unidirectional cDNA library generated from [Pool of
sugarcane calli submitted to low (4oC) and high (37 C)
temperature stress]. cDNA was prepared from polyA+ mRNA
using ZAP - cDNA Synthesis Kit (Stratagene). The
double-strand cDNAs were fractionated in a sepharose CL-2B
40cm-columns and fragments sizing between 0.8 and 1.5 Kb
were directionally cloned into the vector. Details of
each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
'db_xref="taxon:4547"
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888.00
96.7%
96.7%
39.3%
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Indels:
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TITLE
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Pred. No.:
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                                                                                                                                            US-10-601-319-10 (1-432) x CF326092 (1-595)
                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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CP326092
CP326092
CP326092.1 GI:33800445
S EST.
Oryza sativa (japonica cultivar-group)
ISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Enthartoideae; Oryzae; Oryza.

1 (bases 1 to 595)
                                                                      595
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1 (Dases 1 to 595)
1 (Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le Kim,J.S., Jun,K.M., Kim,Y.-K. and Nahm,B.H. Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics and Genetics Institute, ( of Bioscience and Bioinformatics, Yongin, Kyeonggi, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Large-scale Sequencing Analysis
Unpublished (2003)
Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yongin, Kyeonggi, K
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                    AGCGATAACAGCCAGTGGATTCAGGTTTCGCTGGTCTTCCAGACTTTACAGCANATGCGT 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGlnGlnMetArg 383
 GCCACCCCGTTATTAGATTTGATCAAGACAGCGTTGACGCCCCATCCACCGCAAAAACAG
                    AlaThrProLeuLeuAspLeuIleLysThrAlaLeuThrProHisProProGlnLysGln
                                                                                           SerLeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrProGluValAlaArgSerArg
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Nackdong"
/db xref="taxon:39947"
/clone="JMT1 --05-B09"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                            /dev_stage="14 days after germination"
/lab_host="L.coli SOLR"
/clone_lib="AtJMT-overexpressing transgenic rice lambda
/clone_lib="AtJMT-overexpressing transgenic rice lambda
phage cDNA library (JWT1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/NOI; cDNA was inserted into lamda Uni-ZAP XR vector at
end with EcoRI and 3' end with NOI site. mENA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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ool_type="mRNA"
                                                                                                                                                                                               2.93e-75
847.00
99.4%
99.4%
37.5%
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Matches:
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, MyongJi University
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CN762997/c
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                                                                                                                                                                              UNR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Pax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR PRImers
FORWARD: CAGGAAACAGCTATGACC
Plate: 5 row: C column: 9.
                                                                                                                                                                                                                                                                                                                                                                                    Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Acyrthosiphon pisum
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta;
Reoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 895)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Mu
Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN762997
CN762997.1 GI:47536920
EST
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IDOAAA5DCO9RM1 ApMS
                                                                                                                                                                                                                                                                                                                       INRA Rennes
                                                                                                                                                                                                                                                                                                                                    Contact: D.
                                                                                                                                                                                                                                                                                                                                                 Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tags database for
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: }
/sample name: IDOAAA ; Plant growth place: Department
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/dev_stage="nymphs and adults (parthenogenetic
/lab_host="xil-Blue"
                                                                                                                                                                row: C column: 9.
Location/Qualifiers
                                                                                                 /organism="Acyrthosiphon pisum"
|mol_type="mRNA"
/cultivar="developmentstage"
|db_xref="taxon:7029"
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Acyrthosiphon
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SOURCE
ORGANISM
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VERSION
KEYWORDS
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Best Local Similarity:
Query Match:
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5', mRNA sequence.
CN754382
CN754382.1 GI:47519379
EST.
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Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 868)
Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyrthosiple
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839.00
99.4%
99.4%
37.2%
                                                                                                                                                                                                                                                                868 bp
Acyrthosiphon
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Matches:
Conservative:
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Indels:
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pisum cDNA clone
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IDOAAA12DE01
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pea aphid Acyrthosiphon

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score:
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Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORWARD: CAGGAAACAGCTATGACC
Plate: 12 row: E column: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300
LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln
                                                                                  GlnMetArgAspLysThrProLeuSerLeuAsnThrProProGlyGluValLysLeuThr
                                                            CAGATGCGTGATAAAACGCCGCTGTCATTAAATACGCCGCCCGGAGAGGGTGAAACTGACC
                                                                                                                                                                    ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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                                                                                                                                                                                                                                                                                                          PheIleAlaGlyHisAspThrAsnLeuAlaAsnLeuGlyGlyAlaLeuGluLeuAsnTrp
                                                                                                                                                                                                                                                                                        TTTATCGCCGGACACGATACTAATCTGGCAAATCTCGGCGGCGCACTGGAGCTCAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;
Sample name: IDDAPA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction.; experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"
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/mol_type="mRNA"
/cultivar="developmentstage"
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/lab_host="XL1-Blue"
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/tissue_type="whole insect"
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Conservative:
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RESULT 8
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Query Match:
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 864)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

Stern, D., Tagu, D. and Wincker, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMR B103P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2004)
Contact: D. Tagu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acyrthosiphon pisum (pea aphid)
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ThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAlaLeu 301
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                                                                                                                                                                                                                                                                                                           /note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: IDDAAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Harvesting date: 01/06/1999; Stress date: no stress; Description: Aphids inoculated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
/clone_lib="ApMS"
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'cultivar="developmentstage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IDOAAA1DF09"
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                                                                                                                                                                     Mismatches:
                                                                                                                                               Indels:
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Lycopersicon esculentum
Elkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
1 (bases 1 to 383)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holl,I.E., Liang,F., Upton,J., Romning,C.M., Craven,M.B.,
Pujii,C.Y., Bowman,C.L., Mierman,W., Praser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato seed tissue
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383 bp mRNA linear EST 18-MAY-2001 EST274508 tomato seed, TAMU Lycopersicon esculentum cDNA clone cLEE1E23 similar to periplasmic phosphoanhydride phosphohydrolase precursor, putative, mRNA sequence.

AW036132

AW036132.1 GI:5894811
                                                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
101 Jordan Hall, Clemson, SC 29634, USA
101 Jordan Hall, Clemson, SC 29634, USA
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/db_xref="taxon:4081"
/clone="cle81823"
/tissue_type="seeds"
         /dev stage="quiescent seed"
/lab_host="XL1-Blue MRF",
/clome lib="tomato seed, TAMU"
/note="Vector: pBlueScript SK(-); Site 1: EcoR1; Site
Xhol; cLEB - Tomato Seed EST Library. Directionally cl
CDNAs inserted into pBlueScript SK(-) at 5' end with
ECORI and 3' end with XhoI site."
                                                                                                                                                                                  organism="Lycopersicon/mol_type="mRNA"
                                                                                                                                                                                                                              ocation/Qualifiers
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html

prime

sequence.

/mol_type="mRNA" /cultivar="TA496" /db_xref="taxon:4081" /clone="cLEE1E23"

organism="Lycopersicon" ocation/Qualifiers Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 383)
1 (bases 1 to 383)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B.,
Fujil, C.Y., Bowman, C.L., Nieman, W., Fraser, C.M., Venter, J.C.,
Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato seed tissue
                                                                                                                                                                                                                                                                                          AW036134
383 bp mRNA linear EST 18-MAY-200
EST274510 tomato seed, TAMU Lycopersicon esculentum cDNA clone
CLES1E23 similar to periplasmic phosphoanhydride phosphohydrolase
precursor, putative, mRNA sequence.
AW036134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAATGCTGACGGAGATATTT
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RESULT 11
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                           M11B12STM Arabidopsis developing seed clone M11B12 5', mRNA sequence.
BE520240
                                   Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University,
                                                                                                                                       1 (bases 1 to 393)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Vilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
Cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnalaAspThrSerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGln 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAACAGGCGAAGCCTTCGCCGGCCGGGCTGGCACCTGACTGTGCAATAACCGTACATACC
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Xho1; CLEE - Tomato Seed EST Library. Directionally cloned
cDNAs inserted into pBlueScript SK(-) at 5' end with
EcoRI and 3' end with XhoI site."
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Arabidopsis thaliana
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RST.
Schistosoma japonicum
Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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Email: benning@msu.edu

Michigan State University DNA Sequencing Facility Arabidopsis

Biological Resource Center, The Ohio State University, 309 Bot

Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                    BU713769 531 bp mRNA linear EST 23-OCT-200 SJAABUGO1 Adult SjC 7/94 Schistosoma japonicum cDNA similar to sp|P07102|PPA ECCLI PERIPLASNIC APPA PROTEIN PRECURSOR (INCLUDES: PHOSPHOANHYDRĪDE PHOSPHOHYDROLASE (PH 2.5 ACID PHOSPHATĀSE) (AP);
                                                                                    BU713769
BU713769.1
                                                                                                                      6-PHYTASE ], mRNA sequence.
                                                                                                                                                                                                                                                                                  ValSerLeuThrGlyAlaValSerLeuAlaSer 237
                                                                                                                                                                                                                                                                                                                                                                                                                     GluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGln
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                                                                                                                                                                                                                                                                                                                                                                                                 GAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGCCTTAAACGTGAGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAGCAGGGCAGGGGTCAATTGCTGACTTTACCGGGCATCGGCAAACGGCGTTTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: p'
Site_1: EcoRI; Site_2: XhoII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="seed"
/dev_stage="5-13 days
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ecotype="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis
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621.00
95.4%
94.7%
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                                                                                      GI:28321125
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Query Match:
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 531)
Hu,W. Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
Xu,X.N., Wang,S.Y., Chen,Z. and Han,Z.G.
Bvolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                   AlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThrGluIlePhe
                      LeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThrAspSerHis 263
                                                                                                   GCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACGGAGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /uev_brugger_Adult worms
//lab_host="Mouse and rabbit"
/clone_lib="Adult $jc 7/94"
/clone_lib="Adult $jc 7/94"
/clone_lib="Adult $jc 7/94"
/note="Vector: Lambda ZaP-II XR.; Site_1: EcoR I; Site_2:
Xhol I; Several hundred adult Schistosoma japonicum
(Anhui, P.R. China, strain), of mixed sex, were perfused
from the mesenteries of experimentally infected mice and
rabbits at the Queensland Institute of Medical Research,
Brisbane, Australia (QIMR), and stored for several months
in liquid nitrogen. Subsequently, mRNA was isolated at the
QIMR from lysates of these worms by oilgo dT
chromatography, using a kit from pharmacia. The mRNA was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
then shipped to Clontech, Palo Alto, CA, USA, who
constructed a cDNA library. First strand synthesis was
primed with an oilgo-dT-XhoI-primer and synthesis was
accomplished with RNASE H and T4 DNA polymerase. The
double stranded cDNA was ligated to EcoRI linkers,
digested with EcoRI and XhoI, and ligated into the
phagemid vector lambda ZAP II XR. After construction of
this directional library by Clontech, it was returned to
the QIMR. During analysis of the library at the QIMR, we
have found that a small percentage, 2% to 3%, of the
clones contain inserts that appear to be highly homologous
to sequences from salmonoid fishes, as determined by
homology commarisons using BLAST and by Southern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology comparisons using BLAST and by Southern by hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain S. japonicum sequences."
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Whole body"
/dev_stage="Adult worms"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6182"
/sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Chinese (Anhui) strain"
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75.6%
25.8%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       706 bp mRNA linear EST 20-MAY-2004 IDOAAA24BC04RM1 ApMS Acyrthosiphon pisum cDNA clone IDOAAA24BC04 CN759004 CN759004 CN759004.1 GI:47532927
                                                                                                                                                                                                                                                                                                                                                                             UMR B103P, BP 35327, F-35653 Le Rheu Cedex France Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory (Buchnera) or facultative endosymbionts. These sequences were obtained in the frame of the International Consortium of Aphid Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B., Stern, D., Tagu, D. and Wincker, P. An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acyrthosiphon pisum (pea aphid)
Acyrthosiphon pisum
Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 706)
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Unpublished (2004)
                                                                                                                                                                                                                                                                                 FORWARD: CAGGAAACAGCTATGACC
Plate: 24 row: C column: 4.
Location/Qualifiers
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INRA Rennes
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/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI; Sample name: IDOAAA; Plant growth place: Department of
                                                                           /tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                              db_xref="taxon:7029"
clone="IDOAAA24BC04"
                                                                                                                                                                                          mol_type="mRNA"
cultivar="developmentstage"
                                                                                                                                                                                                                                        organism="Acyrthosiphon pisum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -CCTTATGGGGAT 512
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TITLE
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AUTHORS
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AA545747/c
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                                                                                                                                                                                                                                                                                          Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon, G., Hillier, L., Allen, M., Bowles, L., Gelsel, S., Kucaba, T. Marra, M., Martin, J., Steptoe, M., Tan, P., Theising, B., Bowers, Y., Wylie, T., Waterston, R., Wilson, R. and Francomano, C. WashU-MGB/NHGRI EST Project
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                        National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda,
                                                                                                                                                                                                                               Medical Genetics Branch
                                                                                                                                                                                                                                                     Contact: Libin Jia
                                                                                                                                                                                                                                                                      Unpublished (1997)
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1 (bases 1 to 354)
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                                                                                il: libin@helix.nih.gov
primer: M13 Reverse.
    Location/Qualifiers
                                                                                                                                               301-402-4877
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Stromal Fibroblast Homo sapiens cDNA
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                 707 bp mRNA linear EST 01-OCT.
BJ619443 NIBB Mochii normalized Xenopus early gastrula library
Xenopus laevis cDNA clone XL189d24 5', mRNA sequence.
BJ619443
                                                  Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshin@genes.nig.ac.jp The information of this clone is availal
                                                                                                                                                               Contact: Tadasu Shin-i
Center For Genetic Res
                                                                                                                                                                                                                                                Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 707)
Kityama, A., Terasaka, C., Mochii, M., Ueno, N
                                                                                                                                                                                                                                                                                                                                                                               BJ619443.1 GI:37258203
EST.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                   Unpublished (2001)
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                                                                                                                                                                                                                   Expressed genes in X. laevis
                                                                                                                                                                                                                                      Kohara,Y
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
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/cell_type="stromal fibroblast"
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/dev_stromale="mixed"
/lab_host="XI1-Blue"
/clone_lib="Human Bone Marrow Stromal Fibroblast"
/note="Vector: pBluescript; Site_1: EcoRI; Site_2:
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Search completed: June Job time : 4899.67 seco	Qy 331 Db 242	Qy 311 Db 182	Qy 291 Db 122	Qy 271 Db 62	Qy 251 Db 2	US-10-601-319-10	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	BOUTCE ORIGIN
leted: June 14, 2006, 15:26:34 489.67 secs	31 AsmLeuGlyGlyAla 335 42 AATCTCGGCGGCGCA 256	11 TyrGlyValThrLeuProThrSerValLeuPheIleAlaGlyHisAspThrAsnLeuAla 330 	91 ThrProLeuLeuAspLeuIleLysThrAlaLeuThrProHisProProGlnLysGlnAla 310 	71 LeuHisAsnAlaGlnPheAspLeuLeuGlnArgThrProGluValAlaArgSerArgAla 290 62 TTGCATAACGCGCAATTTTATTTGCTACAACGCACGCCCAGAGGTTGCCCGCAGCCGCGCC 121	51 MetProGluProGlyTrpGlyArgIleThrAepSerHisGlnTrpAenThrLeuLeuSer 270 ATGCCGGAGCCGGGGTGGGAAGATCACCGATTCACACCAGTGGAACACCTTGCTAAGT 61	19-10 (1-432) x BJ619443 (1-707)	nt Scores: 4.29e-34	1707 /organism="Xenopus laevis" /mol_type="mRNA" /db_xref="taxon:8355" /clone="%tl189624" /tissue_type="whole embryo" /dev stage="stage 10.5" /clone_lib="NIBB Mochii normalized Xenopus early gastrula library"

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MEDLINE=92049231; Pu
Dassa J., Fsihi H.,
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MEDLINE=93256556; PubMed=8387749; DOI=10.1006/abbi.1993.1261;
Greiner R., Konietzny U., Jany K.-D.;
"Purification and characterization of two phytases from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greiner R., Jany K.-D.; "Characterization of a phytase from Escherichia coli."; Biol. Chem. Hoppe-Seyler 372:664-665(1991).
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for a putative third cytochrome oxidase and for pH
phosphatase (appA).";
mol. Gen. Genet. 229:341-352(1991).
       PIR;
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Ostanin K., Harms E.H., Stevis P.E.,
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MBL; U00096; AAC74065.1; -; Genomic_DNA.
MBL; D90735; BAA35745.1; -; Genomic_DNA.
MBL; X05471; CAA29031.1; -; Genomic_DNA.
MBL; M56708; -; NOT_ANNOTATED_CDS; Genomic_DNA.
MBL; M563811; AAB20266.1; -; Genomic_DNA.
MBL; B63831; AAB20266.1; -; Genomic_DNA.
MBL; B36733, B36733.
DB; 1DKM; X-ray; A/B=23-432.
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INDUCTION: In addition to cAMP-mediated control, this enzyme induced when bacterial cultures reach stationary phase; its synthesis is triggered by phosphate starvation or a shift from aerobic to anaerobic conditions.
SIMILARITY: Belongs to the histidine acid phosphatase family.
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CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)0 = 1D-
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CATALYTIC ACTIVITY: A phosphate monoester +
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ID Z3Z8I_SHISS
PRELIMINARY; PRT; 432 A
AC Q3Z3E1;
DT 27-SEP-2005, sequence version 1.
DT 27-SEP-2005, entry version 5.
DE Phosphoanhydride phosphorylase.
GN Name-sppA; OrderedLocusNames=SSO_0987; ORF
OS Shigella sonnei (strain SSO46).
CE Enterobacteria; Proteobacteria; Gammaproteobacte
OC Enterobacteriaceae; Shigella.
OX NCBI_TAXID=300269;
RN WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC D
RX PubMed=16275786; DOI=10.1093/nar/gki954;
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PubMed=16275786; DOI=10.1093/nar/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y.,

Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun

Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z

Qiang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species, the
agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).
   EMBL; CP000038; AAZ87721.1; -; Genomic DNA. GO; GO:003993; F:acid phosphatase activity; InterPro; IPR000560; HisAc Daphse. Pfam; PP00328; Acid phosphat A; 1. PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1. PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOV
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QBGN88;
01-MAR-2003,
01-MAR-2003,
07-FEB-2006,
EMBL; AP537219; AAN28334.1; -; Genomic_DNA.
HSSP; P07102; 1DKM.
SMR; OBGNBB; 23-432.
GO; GO:0003993; F:acid phosphatase activity
InterPro; IPR000560; HisAc_Dhsphtee.
Pfam; PF00328; Acid_Dhosphat_A; 1.
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKN
                                                                                                                                                                                                                                                                                                                                                                   AppA;
Name=appA;
Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
Chen Y., Zhu Z., Zhang Z., He J.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/tuDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                          Zhang Z., He J., Yao
Submitted (AUG-2002)
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ilarity 98.1%;
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D6_ECOLI

Q8RKD6_ECOLI

Q8RKD6;
                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
MEDLINE=93054596; Pu
Ostanin K., Harms E.
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"The complete nucleotide sequence of reveals significant homology between glucose-1-phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UUN-2002, integrated into Unit
01-UUN-2002, sequence version 1.
07-FBB-2006, entry version 13.
Periplasmic phosphoanhydride phos
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    EMBL;
                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                            "Overexpression, site-directed mutagenesis, Escherichia coli acid phosphatase."; J. Biol. Chem. 267:22830-22836(1992).
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MEDLINE=90368616; Pu
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E.H., Stevis P.E.,
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    13.
    de phosphohydrolase

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Pred. No. 1.9e-161;
1; Mismatches 8;
    Genomic_DNA.
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RESULT 5
QBRKD7, E
DB QBRKD7, E
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GN Name-app
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RN (1)
RX MEDLINE-
RA Dassa J.
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SMR; QBRKDG; 23-432.

GO; GO:0003993; F:acid phosphatase activity; IEG; GO:0016787; F:hydrolase activity; IEA.

InterPro; IPR000560; HisAc_phsphtse.
Pfam; P000328; Acid_phosphat A; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT 1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN_PROSITE; PS007788; HIS_ACID_PHOSPHAT 2; UNKNOWN_PROSITE; PS007788; HIS_ACID_PHOSPHAT 2; UNKNOWN_PROSITE; 
                                                                                                                                   NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

MEDLINE=90368616; PubMed=2168385;

MEDLINE=90368616; PubMed=2168385;

Dassa J., Marck C., Boquet P.L.;

"The complete nucleotide sequence of the complete nucleotide sequence of the reveals significant homology between piglucose-1-phosphatase.";

J., Bacteriol. 172:5497-5500(1990).
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01-JUN-2002, sequence version
07-FBB-2006, entry version 13.
Periplasmic phosphoanhydride p
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Enterobacteriaceae; Escherichia.
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Escherichia coli.
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QBRKD7;
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Pred. No. 2.
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pH 2.5 acid phosphatase
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MEDLINE=93054596; PubMed=1429631; Ostanin K., Harms B.H., Stevis P.E.,

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NUCLEOTIDE SEQUENCE.

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RESULT 6
QBRKDB_ECOLI
QBRKDB_ECOLI
D$\overline{\text{QBRKDB_ECOLI}}
PRELIMINARY; PRT; 432 AA.
AC QBRKDB;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 13.
DT 07-FEB-2006, entry version 13.
DE Periplasmic phosphoanhydride phosphohydrolase.
GN Name-appA;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; En OC Enterobacteriaceae; Escherichia.

NCBI TaxID=562;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90368616; PubMed=2168385;
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GO; GO:0003993; F:acid phosphatase activit GO; GO:0016787; F:hydrolase activity; IEP InterPro; IPR000560; HisAc_phsphtse.

Pfam; PF00328; Acid_phosphat_A; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UN Hydrolase.
                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
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"Overexpression, site-directed mutagenesis,
Escherichia coli acid phosphatase.";
J. Biol. Chem. 267:22830-22836(1992).
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Pred. No. 2
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SEQUENCE
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GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; Hisac phsphtse.
Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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HSSP; P07102; 1DXM.
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MEDLINE=93054596; PubMed=1429631;
MEDLINE=93054596; PubMed=1429631;
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J. Bacteriol. 172:5497-5500(1990).
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                                                                                           LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
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RESULT 7

QBRKEO ECOLI PRELIMINARY; P.

LD QBRKEO;

AC QBRKEO;

DT 01-JUN-2002, integrated into Un.

DT 01-JUN-2002, sequence version 1.

DT 07-PEB-2006, entry version 13.

DB Periplasmic phosphoanhydride pho

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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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HSSP; P07102; 1DKM.
SMR; OBKKB0; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisBac_phsphtse.
Pfam; PF00328; Acid_phosphat_A; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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NUCLEOTIDE SEQUENCE.
MEDLINE=93054596; P.
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Chem. 267:22830-22836(1992).
                                                                                                RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
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MEDLINE=90368616; PubMed=2168385;

MEDLINE=90368616; PubMed=2168385;

Dassa J., Marck C., Boquet P.L.;

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HSSP; P07102; 1DKQ.
SMR; QBKD9; 23-432.
GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid phosphat_A; 1.
PROSTIE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
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MEDLINE=90368616; PubMed=2168385;

Dassa J., Marck C., Boquet P.L.;

"The complete nucleotide sequence of th
reveals significant homology between pH
glucose-1-phosphatase.";
J. Bacteriol. 172:5497-5500(1990).
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Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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HSSP; P07102; 1DXM.
SMR; QBRKD5; 23-432.
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MEDLINE=93054596; PubMed=1429631;
Ostanin K., Harms B.H., Stevis P.B., Kuciel R.,
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Escherichia coli acid phosphatase.";
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                                                                                     YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
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PubMed=16775786; DOI=10.1093/nar/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y

Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., S

Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Ya

Qiang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species,"
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Name-apph; OrderedLocusNames-SBD 2250;
Shigella boydii serocype 4 (straIn Sb227).
Bacteria; Proteobacteria; Gammaproteobacteria;
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GO; GO:0003993; F:acid phosphatase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agents of bacillary dysentery.";
Nucleic Acids Res. 33:6445-6458(2005).
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Pred. No. 1.4e-159;
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180 120

180

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AC QB3RW2;

DT 01-JUN-2003, i
DT 05-JUL-2005, e
DE Phosphoanhydri
GN Name-appA, Ord
OS Shigella flexm
OC Enterobacteria
OX NCBI_TAXID=623
RN [1]

RP NUCLEOTIDE SEC
RC STRAIN=301 / S
RX MEDLINE=22722
RA Jin Q, Yuan Z
RA Yang J., Yang
RA Yang J., Yang
RA Sun L., Xue Y.
RA Cheng H., Yao
RA Yang J., Yang
RA Sun L., Xue Y.
RA Cheng H., Yao
RA Cheng H., Yao
RA Cheng H., Yao
RA Sun L., Sue Y.
RA Cheng H., Yao
RA Sun L., Sue Y.
RA Cheng H., Yao
RA Genome sequen
RT through compact
RI LACOSE71
RC COPYTIGHTED U.;
CC COPYTIGHTED U.;
CC COPYTIGHTED U.;
CC DISTITUDE COMPACT
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Matches 418; Conserv
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05-JUL-2005, sequence version
07-FEB-2006, entry version 15.
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Name=appA; Ordered
Shigella flexneri.
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GO; GO:000393; F:acid phosphatease activity; IEA.
InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; Acid phosphat A; 2.
PROSITE; PS00616; HIS ACID PHOSPHAT 1; UNKNOWN 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.
COMPILED PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE005674; AAN42610.2; -; Genomic_DNA. SMR; Q83RW2; 23-432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Shigella.
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MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
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EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
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OrderedLocusNames=SF0982;
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Pred. No. 3.5e-159;
1; Mismatches 13;
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InterPro; IPR000560; Hisac_phsphtse.

Pfam; PF00328; Acid_phosphat A; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT 1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.

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A7042 MW; 71B0E5EEDZEA2674 CRC64;
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MEDLINE=9919454; PubMed=10092520; DOI=10.1006/bbrc.1999.0361;
Rodriguez E., Han Y., Lei X.G.; Par Racherichia coli ac
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05-JUL-2004, sequence version 1.
07-FBB-2006, entry version 8.
Acid phosphatase/phytase 2.
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GO; GO:0003993; F:acid phosphatase activity;
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Biochem. Biophys. Res. Co
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                         YQTAPRELERVLMPPQSMLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT
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STRAIN=24577 / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

DOI=10.1128/IAI.71.5.2775-2786.2003;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A

Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella

flexner1 serotype 2a strain 2457T.";

Infect. Immun. 71:2775-2786(2003).
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GO; GO:0003993; F:acid phosphatase activity; IEA.
GO; GO:0003993; F:acid phosphatee.
InterPro; IPR000560; HisAc phsphtee.
Pfam; PF00328; Acid phosphat A; 1.
PROSITE; PS00616; HIS ACID PHOSPHAT 1; UNKNOWN 1.
PROSITE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1.
SEQUENCE 432 AA; 47136 MW; 200442239BC66DFC CRC64;
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RESULT 14

Q7AFW3_ECOS7
ID Q7AFW3;
AC Q7AFW3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 10.
DT 07-FBB-2006, entry version 10.
DT 07-FBB-2006, entry version 10.
DE Phosphoanhydride phosphorylase.
QN CPGRE-2016, entry version 10.
DE Phosphoanhydride phosphorylase.
QN CPGRE-2016, entry version 10.
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Best Local Similarity
Matches 419; Conserv
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STRAIN-0157:H7 / Sakai / RIMD 0509952 / EHEG.
MEDLINE-21156231; PubMed-11258796; DOI=10.1093/dnares/8.1.11;
HAYASHI T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003993; F:acid phosphatase activity; IEA.
InterPro; IPR000560; HisAc phsphtse.
Pfam; PF00328; Acid phosphat A; I.
PROSTIE; PS00616; HIS ACID PHOSPHAT 1; 1.
PROSTIE; PS00778; HIS ACID PHOSPHAT 2; UNKNOWN 1.
SEQUENCE 434 AA; 47337 MW; F197DF7D1869F9C4 (
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GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFT
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BioCyc; ECOL83334-1:ECS1136-MONOMER; -..

R GO; GO:0003993; F:acid phosphatase activity; IEA.

IN Interpro; IPR000560; HisAc phosphate.

R Pfam; PF00328; Acid phosphat A; 1.

R PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.

R RROSITE; PS00778; HIS_ACID_PHOSPHAT 2; UNKNOWN 1.

Complete proteome.

SEQUENCE 444 AA; 48188 Mm.
                                                                   Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-0157:H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

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Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";

Nature A06520.623 (2001)
                                                                                                                                                                                                                                                                                                        EMBL; AE005174; AAG555528.1; -; Genomic_DNA.
PIR; D85633; D85633.
PIR; H90770; H90770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                              Match
Local Similarity
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MKAILIPFLSLLIPLTPQSAFAQS--EPELKLESVVIVSRHGVRAPTKATQLMQDVTPDA
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llarity 96.5%;
Conservative
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                                                                Score 2144; DB 2;
Pred. No. 9e-159;
0; Mismatches 13;
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                                                RWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGF
                                                                                                                                                                                                                                                                                                                      WPTWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKT
               TQIVNEARIPACSL
                                                                                                                                                                                                                       GHYQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASM
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                                                                                                                                                                                                                                                                             GEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFT
TQIVNEARIPACSL
                                                                                                  IALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFE
                                                                                                                TALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFE
                                                                                                                                                     LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIM
                                                                                                                                                                   LTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIK
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Search completed: June 13, 2006, Job time: 190.248 secs 10:28:33

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Result
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-MODEL-strame+ p2n.model -DEV=xlp
-MODEL-strame+ p2n.model -DEV=xlp
-MODEL-strame+ p2n.model -DEV=xlp
-Q=/abse/ABSSWEB spool/US10601319/runat 12062006 180055 27578/app query.fasta_1
-Q=/abse/ABSSWEB spool/US10601319 -SUPFIX=rni -MINMATCH=0.1 -LOOPEXI=0
-LOOPEXI=0 -UNITS-Bits -START=1 -END=-1 -MATRIX-bloeum62 -TRANS-human40.cdi
-LOSPEXI=0 -UNITS-Bits -START=1 -END=-1 -MAXE-100 -THR MIN-0 -ALIGN=15
-MODE-LOCAL -OUTFWIT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXE-200000000
-HOST=abse30p -USER=US10601319 @CGN 1 1 381 @runat 12062006 180055 27578
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-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -NCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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seq length: 2000000000
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/Backfiles1.seq:*
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Match
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US-09-259-214-1

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-08-764-233A	-09-028-934-	-08-729-21	-08-457-33	-08-764-233A-	-08-458-076A-	-08-457-646	-08-457-342-	-08-456-837	-08-258-261B	-09-955-59	-09-651-941-	-09-655-27	-09-482-55	-08-993-359-	-09-902-540-11	-09-902-540-311	-09-488-265B-	-09-684-855-16	-10-062-848-1	-09-635-504-3	-09-044-718-1	-744-231-3	-08-868-435-3	-08-920-828-2	-08-362-577C-	-08-921-177-2	-08-920-827-2	-08-920-812-2	-09-489-039	-09-489-039A-34	-08-910-79	-09-715-477-	66-041A-	-09-540-149A	-09-715-477-	0000
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ALIGNMENTS

US-09-866-379-7 US-09-866-379-7 ; Sequence 7, Application US/09866379 • Patent No. 6855365

APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith

GRAY, Kevin

RESULT 1

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APPLICANT: O'DONOGHUB, Bileen
ITITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1999-08-13
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ORGANISM: Escherichia coli
                        TYPE: DNA
                                                          ENGTH: 1901
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Query Match:
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Pred. No.:
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NAME/KEY: misc_feature
LOCATION: (1)...(1901)
OTHER INFORMATION: n is any nucleotide
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                                                                                                             LysValSerAlaAspCysValSerLeuThrGlyAlaValSerLeuAlaSerMetLeuThr 240
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ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla 300
                                 AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln 280
                                                                                                                                                                                    CGGCAAACGGCGTTTCGCGAACTGGAACGGGTGCTTAATTTTCCGCAATCAAACTTGTGC
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                                                                                                    AAGGTGAGCGCCGACAATGTCTCATTAACCGGTGCGGTAAGCCTCGCATCAATGCTGACG
                                                                                                                                             CTTAAACGTGAGAAACAGGACGAAAGCTGTTCATTAACGCAGGCATTACCATCGGAACTC
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Conservative:
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APPLICANT: GRAT, NEVAL

APPLICANT: GARRETT, James

APPLICANT: GARRETT, James

APPLICANT: O'DONOGHUE, Elleen

ITILE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND

FILE REFERENCE: DIVER1370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT FILING DATE: 2001-05-24

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,791

PRIOR APPLICATION NUMBER: US 09/291,791

PRIOR APPLICATION NUMBER: US 09/291,791

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.1

SEQ ID NO 9

LENGTH: 1901
                                                                                                                            ; ORGANISM: Escherichia coli
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1901)
; OTHER INFORMATION: n is any
US-09-866-379-9
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Patent No. 6855365
GENERAL INFORMATION:
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APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
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                                   ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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GENERAL INFORMATION

APPLICANT: DIVERSA CORPORATION

APPLICANT: SHORT, Jay

APPLICANT: SHORT, Keith

APPLICANT: GRAY, Keith

APPLICANT: GRAY, Kevin

APPLICANT: GRAY, Kevin

APPLICANT: GRAY, Kevin

APPLICANT: GRAY, Kevin

APPLICANT: O'DONOGHUB, Sileen

TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEF

FILE REFERENCE: DIVERL370-7

CURRENT APPLICATION NUMBER: US/09/866,379

CURRENT APPLICATION NUMBER: US 09/518,528

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/290,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10

SOPTWARE: PATENTIA 1991

SEQ ID NO 5

LENGTH: 1901

TYPE: DNA

ORGANISM: Becherichia coli

PEATURE:

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Best Local Similarity:
Query Match:
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; OTHER INFORMATION: n is any nucleotide US-09-866-379-5
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APPLICANT: GARRON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1000-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR PRICHING DATE: 1999-05-25
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR PILING DATE: 1997-08-13
PRIOR PILING DATE: 1997-08-13
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
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TYPE: DNA
ORGANISM: Escherichia coli
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                                                              GTGCGTGCTCCAACCAAGGCCACGCAACTGATGCAGGATGTCACCCCAGACGCATGGCCA
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SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,C or G
US-09-259-214-1
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APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: DIVERL370-1
CURRENT APPLICATION NUMBER: US/09/259,214A
CURRENT FILING DATE: 1999-03-01
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
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                                               SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla 160
                                                                                                    AlaPheAlaAlaGlyLeuAlaProAspCysAlaIleThrValHisThrGlnAlaAspThr
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Conservative:
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Sequence 1, Application US/09318528
Patent No. 6183740
GENERAL INFORMATION:
APPLICANT: Kreetz, Keith
FILE REFERENCE: 09010/02903
CURRENT APPLICATION NUMBER: US/09/318,528
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 09/291,931
EARLIER FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1997-08-13
EARLIER FILING DATE: 1999-03-01
INUMBER: OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
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                                           GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                                                                           | SerSerProAspProLeuPheAsnProLeuLysThrGlyValCysGlnLeuAspAsnAla
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     AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
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GENERAL INFORMATION:
APPLICANT: Kretz, Keith
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCE: 09010/029003
CURRENT APPLICATION NUMBER: US/09/291,931A
CURRENT FILING DATE: 1999-04-13
EARLIER APPLICATION NUMBER: 08/910,798
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER APPLICATION NUMBER: 09/259,214
EARLIER FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
                                                      Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                                                                                                                                                                  TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc_feature
LOCATION: (1)...(1321)
OTHER INFORMATION: n = A,T,C
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SEQ ID NO 1

LENGTH: 1323

TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1320)
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n = A,T,(
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TITLE OF INVENTION: NOVEL PHYTASE
TITLE OF INVENTION: NOVEL PHYTASE
FILE REFERENCES: 0910/02903
CURRENT APPLICATION NUMBER: US/09/580,515
CURRENT FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR APPLICATION NUMBER: 09/291,931
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-03-01
NUMBER: 05-25
PRIOR PELLYG DATE: 1999-03-01
NUMBER: PETEN FOR WINDER: VENTIOR APPLICATION NUMBER: 09/259,214
PRIOR FILING DATE: 1999-03-01
NUMBER: PETEN FOR WINDER: VENTIOR APPLICATION NUMBER: 09/259,214
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GlyHisTyrTrpArgGlnArgLeuValAlaAspGlyLeuLeuProLysCysGlyCysPro
                                               ThrTrpProValLysLeuGlyGluLeuThrProArgGlyGluLeuIleAlaTyrLeu
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                                                                                                 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerLeuAlaGlyPheThrGln 420
                                                                                                                                                                        GlnMetArgAspLysThrProLeuSerLeuAsnThrProFroGlyGluValLysLeuThr
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PATENT OIL SESSIES

GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERL370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
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PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
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PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1999-03-01
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1323)
OTHER INFORMATION: n is any nucleotide
NAME/KEY: CDS
LOCATION: (1)...(1323)
OTHER INFORMATION:
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SOFTWARE: PatentIn versionsEQ ID NO 1
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GENERAL INFORMATION:
APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OP INVENTION: SITE-DIRECTED MUTAGENESIS OF ESCHERICHIA COLI PHYTASE
FILE REFERENCE: 19603/4031
CURRENT APPLICATION NUMBER: US/09/715,477
                                                                                                 Sequence 2, Application Patent No. 6841370
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PRIOR APPLICATION NUMBER: 60/166,179
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
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             GluIlePheLeuLeuGlnGlnAlaGlnGlyMetProGluProGlyTrpGlyArgIleThr
                                            AsnValThrAspAlaIleLeuGluArgAlaGlyGlySerIleAlaAspPheThrGlyHis
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                                                                                                       LeuLysArgGluLysGlnAspGluSerCysSerLeuThrGlnAlaLeuProSerGluLeu
                                                                                                                                                      TyrGlnThrAlaPheArgGluLeuGluArgValLeuAsnPheProGlnSerAsnLeuCys
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GENERAL INFORMATION:

APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
FILE REFERENCE: 19603/2791
CURRENT APPLICATION NUMBER: US/09/540,149A
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Escherichia
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 TTCGCTCAGAGTGAGCCGGAGCTGAAGCTGGAAAGTGTGGTGATTGTCAGCCGTCATGGT
              PheAlaGlnSerGluProGluLeuLysLeuGluSerValValIleValSerArgHisGly 40
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CAGATGCGTGATAAAACGCCGCTATCATTAAATACGCCGCCCGGAGAGGTGAAACTGACC
                                                                        ArgArgLeuSerAspAsnSerGlnTrpIleGlnValSerLeuValPheGlnThrLeuGln
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GENERAL INFORMATION:

APPLICANT: Le1, Xingen
ITILE OF INVENTION: PHOSPHATASESS WITH IMPROV
FILE REFERENCE: 19603/2798

CURRENT APPLICATION NUMBER: US/10/266,041A
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: 60/127,032
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR APPLICATION NUMBER: 09/540,149
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
SOPTWARE: PATENTIN VER. 2.1
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Best Local Similarity:
Query Match:
DB:
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TYPE: DNA
ORGANISM: Escherichia
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GENERAL INFORMATION:

APPLICANT: Lei, Xingen
ITILE OF INVENTION: SITE-DIRECTED MUTAGENES
FILE REFERENCE: 19603/4031

CURRENT APPLICATION NUMBER: US/09/715,477

CURRENT FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 06/166,179

PRIOR FILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 9

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 1486

TYPE: DNA

CECANITY
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US-09-715-477-4
; Sequence 4, Application US/09715477
; Patent No. 6841370
; Patent No. 6847370.
 ORGANISM: Escherichia coli
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Best Local Similarity:
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                                              ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
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RESULT 14
US-08-910-798-1
; Sequence 1, Ap
                                                                                                                         APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPAN: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1772 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECTIFE TWOSE: Num (Commail)
Alignment Scores:
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US-08-910-798-1
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Patent No. 5876997
GENERAL INFORMATION:
APPLICANT: KRETZ
TITLE OF INVENTION: NOVEL PHYTAL
                                                                                                                                                                                                                                                                                                                                                             ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                       MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: PHYTASE
FEATURE:
NAME/KEY:
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CORRESPONDENCE ADDRESS:
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                                                                                 ArgThrProGluValAlaArgSerArgAlaThrProLeuLeuAspLeuIleLysThrAla
                                                                                                                          GATTCACACCAGTGGAACACCTTGCTAAGTTTGCATAACGCGCAATTTTATTTGCTACAA
                                                                                                                                              AspSerHisGlnTrpAsnThrLeuLeuSerLeuHisAsnAlaGlnPheAspLeuLeuGln
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILE REPERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 341
LENGTH: 1266
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                                      ACGCTTCCCGGTCAGCCGGATAACACGCCGCCAGGTGGTGAACTGGTGTTTGAACGCTGG
                                                            GlyGlyGluLeuIleAlaTyrLeuGlyHisTyrTrpArgGlnArgLeuValAlaAspGly
                                                                                                                              AspValThrProAspAlaTrpProThrTrpProValLysLeuGlyGluLeuThrProArg
                                                                                                                                                            CTGATCATGAGCCGTCACAACCTGCGTGCGTGCGCCGTTGGCCAATAACGGCAGCGTGCTGGAA
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   LeuLeuProLysCysGlyCysProGlnSerGlyGlnValAlaIleIleAlaAspValAsp 112
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GACCAGGGATTCTGCCCGCTGGAGACCTTTAAAATGGTGATCAACGAGGCG
                                 AlaGlnGlyMetCysSerLeuAlaGlyPheThrGlnIleValAsnGluAla 425
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                                                                                                        SerLeuAsnThrProProGlyGluValLysLeuThrLeuAlaGlyCysGluGluArgAsn 408
                                                                                                                                             CTGATGAAGATTGAGTATGTCTATCAAAGTACCGAGCAACTGCGTAACGCCGACGCGTTA 1149
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                                                                                                                                                                                                                                                                                                                                                       -----GCGAAAGTCACGCTGCTGGTGGAACACGACTCGAATATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrGlnAlaLeuProSerGluLeuLysValSerAlaAspCysValSerLeuThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAsnPheProGlnSerAsnLeuCysLeuLysArgGluLysGlnAspGluSerCysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGACTCCCCGGCGTTTCGCGAGAAAGCGCTGCAGGCGATGGAAAAAAGAGCGCCAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyValCysGlnLeuAspAsnAlaAsnValThrAspAlaIle---LeuGluArgAlaGly 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGTGCATCACCAGCCTCAGATGGGCACCATGGACCCGACCTTCAACCCGGTTATTACC
                                                                         ACCCTGCAGGCCCCGCCGCAGCGGGTCACTCTGGCGCTTAACGGCTGTCCGGTT---GAT 1206
                                                                                                                                                                                                                   ACTCCTATCGGCGGCAAACTGCTGTTTCAGCGCTGGCATGACAGCGCCGGCAATCGCGAT 1089
                                                                                                                                                                                                                                   ThrProProGlyGlyGluLeuValPheGluArgTrpArgArgLeuSerAspAsnSerGln 368
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Search completed: June 14, 2006, 15:34:57 Job time : 248.459 secs

307

CTGGTGACCAGCGGCGAGTGCCCGCCGGAAAACGCGGTTTATGCCTACGCTAACAGCCTG

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Maximum Match 10
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                                   seq length: 0
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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                                US-10-601-319-10
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US-10-282-122A-43351
US-10-601-319-8
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US-11-018-709-3
US-10-021-723A-13
US-10-021-723A-13
US-10-021-723A-13
US-10-021-723A-15
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                                                     Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Seque
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426	426	426	118	441	421	409	318	144	476	420	441	441	441	261	432	432	433
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US-10-450-763-53707	US-10-343-357-6	US-10-257-174-44	US-10-450-763-56055	US-11-098-686-10683	US-10-021-723A-6	US-10-021-723A-8	US-10-021-723A-14	US-10-450-763-54615	US-10-021-723A-10	US-10-021-723A-4	US-10-021-723A-2	US-10-282-122A-77792	US-10-021-723A-12	US-10-450-763-56057	US-10-021-723A-16	US-10-284-962-5	US-10-266-041-1
Sequence 53707, A	Sequence 6, Appli	Sequence 44, Appl	Sequence 56055, A	Seguence 10683, A	Sequence 6, Appli	Sequence 8, Appli	Sequence 14, Appl	Sequence 54615, A	Sequence 10, Appl	Sequence 4, Appli	Sequence 2, Appli	Sequence 77792, A	Sequence 12, Appl	Sequence 56057, A	Sequence 16, Appl	Sequence 5, Appli	Sequence 1, Appli

ALIGNMENTS

US-10-601-319-10

Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:

Application US/10601319 vo. US20040091968A1

```
APPLICANT: Gary, Nevan A.

APPLICANT: Gartent, James B.

APPLICANT: Gartent, James B.

APPLICANT: Mathur, Eilen

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: RECOMBINANT PHYTASES AND METHODS OF MAKING FILE REFERENCE: 09010-029011

CURRENT PILING DATE: 2001-05-20

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

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PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR FILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR FILING DATE: 1999-03-01

PRIOR FILING DATE: 1999-03-01

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                                                                                                                                                                                                Query Match 100.0%; Score 2258; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-196; Matches 432; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 43
                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: modified phytase enzyme
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Length 432;
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PRIOR APPLICATION NUMBER: US/09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR PRIOR PELICATION NUMBER: US 09/580,515
PRIOR PELICATION NUMBER: US 09/580,515
PRIOR PELICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/2318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR PELICATION NUMBER: US 09/291,931
PRIOR PELICATION NUMBER: US 09/259,214
PRIOR PELICATION NUMBER: US 09/259,214
PRIOR PELICATION NUMBER: US 08/910,798
PRIOR PELICATION NUMBER: US 08/910,798
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US-10-933-115-10
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Publication No. US20050281792A1
GENERAL INFORMATION:
                                                                                                                            Matches
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                        Query Match
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APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT FILING DATE: 2004-09-01
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                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 432
                                                                                                                                                             Local
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432; Conser
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                          MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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                                                                                                                     100.0%; Score 2258; DB 5; larity 100.0%; Pred. No. 1.8e-196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                  modified phytase enzyme
                                                                                                                                                                                        Length 432;
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APPLICANT: GRATION, Nelson R.
APPLICANT: GARRETT, James B.
APPLICANT: GARRETT, James B.
APPLICANT: O'DONOGHUE, Eilen
APPLICANT: O'DONOGHUE, EILEN
TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PRAYMAKING AND USING THEM
FILE REFERENCE: 564462001803/D1370-9C1
CURRENT FILING DATE: 2005-02-11
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 10/156,660
PRIOR FILING DATE: 2002-05-24
PRIOR RELING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/886,379
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/21,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/29,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
NUMBER OF SER APPLICATION NUMBER: US 08/910,798
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                                                                                       ; OTHER INFORMATION: Modified phytase enzyme US-11-056-354-2
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                                                                                                                                                SOPTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 432; Conservative 0
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Publication No. US20050246780A1
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APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin A.
APPLICANT: BARTON, Nelson
                                                                                                                                  FEATURE:
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Score 2258; DB 6;
Pred. No. 1.8e-196;
); Mismatches 0;
                                          Length
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GENERAL INFORMATION

APPLICANT: Short, Jay M.

APPLICANT: Kretz, Keith

APPLICANT: Gray, Kevin A.

APPLICANT: Garyett, James B.

APPLICANT: Garyett, James B.

APPLICANT: Garyett, James B.

APPLICANT: Garrett, James B.

APPLICANT: Mathur, Eric J.

TITLE OF INVENTION: PATASES, NUCLEIC ACIDS ENCITIES OF INVENTION: PATASES, NUCLEIC ACIDS ENCITIES OF INVENTION: AND METHODS FOR MAKING AND PILE REFERENCE: 09010-029007

CURRENT APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/860,515

PRIOR APPLICATION NUMBER: US 09/80,515

PRIOR APPLICATION NUMBER: US 09/318,528

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-04-13

PRIOR FILING DATE: 1999-08-13

NUMBER OF ESG ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 436
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US-10-156-660-2
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Publication No. US20030103958A1
OTHER INFORMATION: modified phytase enzyme 10-156-660-2
                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                              ENGTH: 436
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APPLICANT: BARTON, Nolson
APPLICANT: GARRETT, James
APPLICANT: GYDNOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVERI370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR PRILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR PRILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/21,931
PRIOR PILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/297,931
PRIOR APPLICATION NUMBER: US 09/297,931
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PRIOR APPLICATION NUMBER: US 09/297,931
PRIOR APPLICATION NUMBER: US 09/297,931
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/297,931
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1997-08-13
NUMBER OF SEO ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified phytase
US-09-866-379-10
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US-09-866-379-10
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                                                                                                          SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 430
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Pred. No. 1.8e-196;
D; Mismatches 0;
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Kevin
APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
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APPLICANT: GARRETT, James
APPLICANT: GARRETT, James
APPLICANT: O'DOCGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILER REFERENCE: DIVER1370-7
CURRENT PEPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
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US-09-866-379-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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98.1%;
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  Score 2182; DB 3; Pred. No. 1.5e-189;
                         Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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       Query Match
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; TYPE: PRT
; ORGANISM: Be
US-10-156-660-4
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson
APPLICANT: Barton, Nelson
                                                                                                                                                                                                            APPLICANT: BATCON, Nelson R.
APPLICANT: Garrett, James B.
APPLICANT: Garrett, James B.
APPLICANT: O'DONOShue, Eileen
APPLICANT: Mathur, Eric J.
TITLE OF INVENTION: AND METHODS FOR MAKING AND METHODS FOR MAKING AND METHODS FOR MAKING AND METHODS FOR MAKING AND METHODS FOR MAKING AND METHODS FOR MAKING AND METHODS FOR MAKING AND METHOD FOR MAKING AND METHOD METHOD MITTER 2001-0-1
PRIOR PILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR PILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/259,214
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                                                             NUMBER OF SEQ ID NOS:
SOPTWARE: FastSEQ for
SEQ ID NO 4
LENGTH: 432
                                                                                                                                                 PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR FILING DATE: 1997-08-13
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Score

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APPLICANT: Maing Daniel
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Obleen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Nu, H.
TITLE OF INVENTION: Identification of Essential Genes in P
FILE REFERENCE: ELITEN, 034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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         APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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US-10-601-319-
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APPLICANT: Barton, Nelson Robert
APPLICANT: Garrett, James B.
APPLICANT: O' Donoghue, Eileen
APPLICANT: Mathour, Eric J.
TITLE OF INVENTION: RECOMBINANT PHYTASES AN
TITLE OF INVENTION: AND USING THEM
FILE REFERENCE: 09010-029011
CURRENT APPLICATION NUMBER: US/10/601,319
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/866,379
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
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US-10-282-122A-43351
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Best Local S
Matches 424
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APPLICANT: Short, Jay M.
APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10601319 Publication No. US20040091968A1
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LENGTH: 432
TYPE: PRT
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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Pred. No. 1.5e-189;
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300

180 180 240

240

120

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Sequence 41, Application US/10472317
Publication No. US20040185562A1
GENERAL INFORMATION:
APPLICANT: Cargill, Incorporated
TITLE OF INVENTION: Myo-Inositol Oxygenases
FILE REFERENCE: 10829/003US1
CURRENT APPLICATION NUMBER: US/10/472,317
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/US02/08404
PRIOR FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR APPLICATION NUMBER: US 60/277,148
PRIOR FILING DATE: 2001-03-19
VNUMBER OF SEG ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH. 412
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US-10-472-317-41
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; TYPE: PRT
; ORGANISM: Escherichia
US-10-601-319-8
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Best Local Similarity
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              ORGANISM: Escherichia coli
                             LENGTH: 432
TYPE: PRT
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Pred. No. 1.5e-189;
0; Mismatches 8;
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APPLICANT: BAILOU, MELON, MELON, APPLICANT: APPLICANT: Garrett, James B.

APPLICANT: O' DONOGHUE, Eileen
APPLICANT: O' DONOGHUE, Eileen
APPLICANT: Mathur, Eric J.

FITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
TITLE OF INVENTION: THEREOF
FILLE REFERENCE: 564462001822
CURRENT APPLICATION NUMBER: US/10/933,115
CURRENT APPLICATION NUMBER: US 09/9866,379
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
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PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 432
; TYPE: PRT ; ORGANISM: Escherichia US-10-933-115-8
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US-10-933-115-8
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Publication No. US20050281792A1
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Best Local Similarity
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APPLICANT: Kretz, Keith A.
APPLICANT: Gray, Kevin A.
APPLICANT: Barton, Nelson Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION
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Pred. No. 1.5e-189
0; Mismatches 8
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APPLICANT: GRAY, KEVIN A.

APPLICANT: BARTON, Nelson R.

APPLICANT: GARRETT, James B.

APPLICANT: GARRETT, James B.

APPLICANT: GARRETT, James B.

APPLICANT: GARRETT, James B.

APPLICANT: MATHUR, Eric J.

TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM AND TITLE OF INVENTION: POR MAKING AND USING THEM FILE REFERENCE: 564462001803/D1370-9C1

CURRENT APPLICATION NUMBER: US/11/056,354

CURRENT FILING DATE: 2005-02-11

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/866,379

PRIOR APPLICATION NUMBER: US 09/860,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/580,515

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR FILING DATE: 1999-05-25

PRIOR PILING DATE: 1999-05-25

PRIOR APPLICATION NUMBER: US 09/291,931

PRIOR APPLICATION NUMBER: US 09/29,214

PRIOR APPLICATION NUMBER: US 09/29,214

PRIOR APPLICATION NUMBER: US 09/259,214

PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR APPLICATION NUMBER: US 08/910,798

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PRIOR APPLICATION NUMBER: US 08/910,798
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US-11-056-354-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHORT, Jay M.
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin A.
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Pred. No. 1.5e-189;
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APPLICANT: Lei, Xingen
APPLICANT: Lei, Xingen
FILE OF INVENTION: SITE-DIRECTED MUTAGENESIS OF
FILE REFERENCE: 19603/403;
CURRENT APPLICATION UNMER: US/11/018,709
CURRENT FILING DATE: 2004-12-20
PRIOR APPLICATION NUMBER: US/9/715,477
PRIOR FILING DATE: 2000-11-79
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIAL Ver. 2.1
SEQ ID NO 1
LENGTH: 432
TYPE: PRT
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                              ; ORGANISM: Escherichia
US-11-018-709-1
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US-11-018-709-1
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                                                                                                                 Matches 423;
                                                                                                                                               Query Match
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TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
                                                                  MKAILIPPLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
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                                                                                                             96.4%;
ilarity 97.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      432
                                                                                                             Score 2177; DB 6;
Pred. No. 4.3e-189;
0; Mismatches 9;
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                                                                                                                                           Length 432;
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FILE REFERENCE: DIVERI370-6
CURRENT APPLICATION NUMBER: US/09/777,566A
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR FILING DATE: 1999-05-25
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
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PRIOR APPLICATION NUMBER: US 08/910,798
PRIOR APPLICATION NUMBER: US 08/910,798
                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n is any nucleotide
US-09-777-566A-2
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US-09-777-566A-2
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09777566A Patent No. US20010055788A1
                                                                                                                                                                                                                                                                  Matches 422;
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 440
                                                                                                                                                                                                                                                                                              Local Similarity
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AFAAGLAPDCAITVHTQADTSSPDFLFNFLKTGVCQLDNANVTDAILERAGGSIADFTGH
                                                                                                TWPVXLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE
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                                                                          TWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGE
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                                                                                                                                                                                                                                                                                      96.1%;
97.7%;
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                                                                                                                                                                                                                                                                                      Score 2171; DB 3;
Pred. No. 1.6e-188;
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                            Length 440;
                                                                                                                                                                                                                                                                  Indels
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APPLICANT: DIVERSA CORPORATION
APPLICANT: SCORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: GRAY, Welson
APPLICANT: GARRETT, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: O'DONOCHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND
FILE REFERENCE: DIVER1370-7
CURRENT APPLICATION NUMBER: US/09/866,379
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 09/580,515
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR APPLICATION NUMBER: US 09/318,528
PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/291,931
PRIOR APPLICATION NUMBER: US 09/297,214
PRIOR APPLICATION NUMBER: US 09/259,214
PRIOR FILING DATE: 1999-03-01
PRIOR PILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 10
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US-09-866-379-2
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 422; Conserv
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09866379 Patent No. US20020136754A1
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 440
TYPE: PRT
ORGANISM: Escherichia coli
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                                                                                                                                                                                                                                                 1 MKAILIPFLSILIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YQTAFRELERVLNPPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH 180
                                                                                                                    TWPVKLGELTPRGGELIAYLGHYWRQRLVADGLLPKCGCPQSGQVAIIADVDERTRKTGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360
                                                         AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILERAGGSIADFTGH 180
                                                                                                                                                                                                                        MKAILIPPLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVNEARIPACSL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLLDLIKTA
                             AFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVNEARIPACSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                   96.1%;
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                 Score 2171; DB 3;
Pred. No. 1.6e-188;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                            Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND USES THEREOF
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                    <u>.</u>
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	IVNEARIPACSL 432	421	8
120	361 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420	361	몽
120	361 RRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQ 420	361	ई
360	301 LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360	301	문
360	301 LTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERW 360	301	8
300	BIFLLQQAQGMPEPGMGRITDSHQMNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIMAA 300	241	문
300	241 BIFLLQQAQGMPBPGWGRITDSHQWNTLLSLHNAQPDLLQRTPEVARSRATPLLDLIKTA 300	241	Ś
240	181 RQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLT 240	181	밁
240	181 YQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240	181	ફ

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